

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:53:30 ; Search time 8133.32 Seconds
(without alignments)
11558.757 Million cell updates/sec

Title: US-10-735-098-3
Perfect score: 2169
Sequence: 1 atgtgtaaacgaattatgg.....tcaggagggtggaataatga 2169

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEnbl:*

1: gb.ba:*

2: gb.htg:*

3: gb.in:*

4: gb.om:*

5: gb.ov:*

6: gb.pat:*

7: gb.ph:*

8: gb.pl:*

9: gb.pr:*

10: gb.ro:*

11: gb.sts:*

12: gb.sy:*

13: gb.un:*

14: gb.vi:*

15: em.ba:*

16: em.fun:*

17: em.in:*

18: em.in:*

19: em.mu:*

20: em.or:*

21: em.or:*

22: em.ov:*

23: em.pat:*

24: em.ph:*

25: em.pl:*

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27: em.sts:*

28: em.un:*

29: em.vi:*

30: em.htg.hum:*

31: em.htg.inv:*

32: em.htg.other:*

33: em.htg.mus:*

34: em.htg.pln:*

35: em.htg.rod:*

36: em.htg.mam:*

37: em.htg.vrt:*

38: em.sy:*

39: em.htgo.hum:*

40: em.htgo.mus:*

41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	100.0	2169	2169	1	AF123382	AF123382 Neisseria
2	100.0	2169	2169	6	A98970	A98970 Sequence 3
3	100.0	2169	2169	6	BD074756	BD074756 Neisseria
4	1562.4	72.0	2124	1	AF123383	AF123383 Neisseria
5	1562.4	72.0	2124	6	A98976	A98976 Sequence 9
6	1562.4	72.0	2124	6	BD074759	BD074759 Neisseria
7	1454.2	67.0	326301	1	NMA622491	AL162257 Neisseria
8	1453.6	67.0	2519	1	AF072890	AF072890 Neisseria
9	1375.8	63.4	2226	1	AF123380	AF123380 Neisseria
10	1375.8	63.4	2226	6	A98972	A98972 Sequence 5
11	1375.8	63.4	2226	6	BD074757	BD074757 Neisseria
12	1360.8	62.7	9955	1	AE002504	AE002504 Neisseria
13	1360.8	62.7	349980	6	AX044033	AX044033 Sequence
14	1304.8	60.2	2277	1	AF022781	AF022781 Neisseria
15	1304.8	60.2	2277	6	A98968	A98968 Sequence 1
16	1304.8	60.2	2277	6	BD074755	BD074755 Neisseria
17	1304.8	60.2	5691	1	AF049349	AF049349 Neisseria
18	1301.6	60.0	2537	1	AF031432	AF031432 Neisseria
19	1250.6	57.7	2262	1	AF123381	AF123381 Neisseria
20	1250.6	57.7	2262	6	A98974	A98974 Sequence 7
21	1250.6	57.7	2262	6	BD074758	BD074758 Neisseria
22	439.2	20.2	1000	6	AX081510	AX081510 Sequence
23	439.2	20.2	1000	6	AX374691	AX374691 Sequence
24	222.4	10.3	3398	1	NMLBPAG	X79838 N.meningiti
25	105.2	4.9	3720	14	S76368	S76368 ORF 5' of E
26	105.2	4.9	43658	14	HSV3PRGEN	M86409 Herpesvirus
27	105.2	4.9	112930	14	HSV3PRGEN	X64346 Salmirine
28	105.2	4.9	214836	10	AC007305	AC007305 Mus muscu
29	105	4.8	232224	2	AC110149	AC110149 Rattus no
30	105	4.8	251960	2	AC107279	AC107279 Rattus no
31	104.6	4.8	194060	2	AC125897	AC125897 Rattus no
32	104.4	4.8	183250	2	AC095977	AC095977 Rattus no
33	103.8	4.8	271336	2	AC111017	AC111017 Mus muscu
34	103.6	4.8	244595	2	AC095144	AC128669 Mus muscu
35	103.4	4.8	169571	10	AC128669	AC122128 Mus muscu
36	103.4	4.8	217150	2	AC122128	AC128669 Mus muscu
37	103.4	4.8	224344	10	AL606969	AL606969 Mouse DNA
38	103.4	4.8	227411	10	AC130821	AC130821 Mus muscu
39	103.4	4.8	230940	10	AC123043	AC123043 Mus muscu
40	103.2	4.8	186134	10	AL591390	AL591390 Mouse DNA
41	103.2	4.8	214019	2	AC064803	AC064803 Mus muscu
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43	103	4.7	226051	2	AC098525	AC098525 Rattus no
44	103	4.7	259653	2	AC108960	AC108960 Rattus no
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ALIGNMENTS

RESULT 1									
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LOCUS									
DEFINITION	AF123382	2169 bp	DNA	linear	BCT 24-MAY-1999				
	Neisseria meningitidis strain m981	lactoferrin-binding protein precursor (lbpb) gene, complete cds.							
ACCESSION	AF123382								
VERSION	AF123382.1	GI:4884690							
KEYWORDS									
SOURCE	Neisseria meningitidis								
ORGANISM	Neisseria meningitidis								
	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;								
	Neisseriaceae; Neisseria.								
REFERENCE	1 (bases 1 to 2169)								
AUTHORS	Petterson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tommassen,J.								

TITLE Sequence variability of the meningococcal lactoferrin-binding protein lbpB
JOURNAL Gene 231 (1-2), 105-110 (1999)
MEDLINE 99250255
PUBMED 10231574
REFERENCE 2 (bases 1 to 1169)
AUTHORS Petersson, A., van der Biesen, J., Jørgensen, V., Hendriksen, J. and Tomassen, J.
TITLE Direct Submision
JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
FEATURES
source location/Qualifiers
1..2169 /organism="Neisseria meningitidis"
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/strain="m981"
/db_xref="taxon:487"
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/codon_start=1
/transl_table=11
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/protein_id="AAD31770.1"
/db_xref="GI:4884691"
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ORIGIN
Query Match 100.0%; Score 2169; DB 1; Length 2169;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGTGTAACCGAATTATGCGGCATTTGTTTGGCCCTTACTTTTGGCATCTTGCATC 60
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DB 121 TTCAAGTCTAAGACGTTCCCTTCCGCCCCCTGCGGGTCTTCGGTAGAAGAACCGCGG 180
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DB 241 CGTGAAGATGGCAGCGCAATTCCTCGATAGCAACACGAGCAAGAAAGCTGCTTTTAA 300
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DB 481 GAGAAAAATCGGATGAAAAAGCAAGTTTCTAATCGTTTAGCTATGAGCGTTTGTATAT 540
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DB 541 TATCTCGGAGAACATCTTCCCAATCTTACCGAGCGGGGAAACGGTCAAAATATTCGGCG 600
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DB 721 GATGCCGATGCGCGGAAAAACATCTCCGCAATATACGGTTAAATTCGACAAAAAATC 780
QY 781 CTGGAAGCTAAGTTGATTAAAAATCAGTATGTGCAAAAGAGAGATGATCCTAAAAATCCA 840
DB 781 CTGGAAGCTAAGTTGATTAAAAATCAGTATGTGCAAAAGAGAGATGATCCTAAAAATCCA 840
QY 841 CTGACCAATTTCAACATTTACCGCAACATTTGACGCGCAACCGCTTTACCGGAGTCCCAA 900
DB 841 CTGACCAATTTCAACATTTACCGCAACATTTGACGCGCAACCGCTTTACCGGAGTCCCAA 900
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DB 901 GTTACACCGAGTCAAGACGCAACACGCTGATAAAGATATTTGTTTTCATACCCGAT 960
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DB 961 GCGGATCAGCGGCTTTGAGGCGGCTTTTTCGCGCATACGAGAGAGAGCTTGC CGGCGG 1020
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DB 1021 TTTTATCAGTAACGACGAGCTATTCGCGCTTTTCGAGGCAACAAAAACAGAGACA 1080
QY 1081 GCAACGCGATCAGATACAAATCTTCCTCCCTGCGCTCTGGAAGAACACACCAAAATCTTGGAT 1140
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DB 1321 TCGATTTTCTGACCTATGTGAAATCTCGGACGGAATAAAACCGACCGCGCGCGCTCAAA 1380
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DB 1381 CCGAAGCGCGAGATCAAGAGGATTCGGACATTTGATATGCGCAAGAAAGCGAAGCGAA 1440
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DB 1441 ATTTCCGAAGATGATAACCGCGAGAGATGAAGTCAACGAGAGAGAGTGAAGAAC 1500
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Db	721	GATCGCGATGGCCGGGAAAAA	CATCTCTGCCGAATATACGGTTAATTTTCGACAAAAAAAC	780
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Db	781	CTGGAAGGTAAAGTTGATTAAAAAT	CAGTATGTGCAAAAGAGAGATGATCTCTAAAAATCCA	840
Qy	841	CTGACCATTTAACAATTTACCGCA	CATTTGGACGGCAACCGCTTTACCGCGAGTGCCCAA	900
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Db	1081	GCAACGCATCAGATACAAATCT	CTGCCCTCTGGAATAACACCAAAATCTTGAT	1140
Qy	1141	TTCTCTAAAATTTCCGTTGACG	AGGCACTGATGACCATGCCGTAAGTTGCCATTCC	1200
Db	1141	TTCTCTAAAATTTCCGTTGACG	AGGCACTGATGACCATGCCGTAAGTTGCCATTCC	1200
Qy	1201	ACTATGCCGATTTTGGTTCAT	CCCGACAACTTTCTTTCGAAGGGCGTGAATTCCTTTG	1260
Db	1201	ACTATGCCGATTTTGGTTCAT	CCCGACAACTTTCTTTCGAAGGGCGTGAATTCCTTTG	1260
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RESULT 3	BD074756	2169 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD074756				
DEFINITION	Neisseria lactoferrin-binding protein.				
ACCESSION	BD074756				
VERSION	BD074756.1	GI:22620359			
KEYWORDS	JP 2001514894-A/2.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	1 (bases 1 to 2169)				
AUTHORS	Felnholm, A.M.P. and Thomassen, J.P.M.				
TITLE	Neisseria lactoferrin-binding protein				
JOURNAL	Patent: JP 2001514894-A 2 18-SEP-2001;				
	UNIVERSITY OF UTRECHT, TECHNOLOGY FOUNDATION				
COMMENT	OS Unidentified				
	DN JP 2001514894-A/2				

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ORIGIN
Query Match          100.0%; Score 2169; DB 6; Length 2169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2169; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 1  ATGTGTAAACCGGAATTATGCGGCAATGTCCTTGTGGCCCTTATCTTTTGGCACTCTTGCATC 60

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Db	661	GATTTGGGTATACCAATATATGTTAATGAAATGCGGAGTAAAGGGGTTTCCAGTG	720
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Db	901	GTTTAGACCGGAGGTGAAGACCAACCGCTGATTAAGAATATTTGTTTTTCCATACCGAT	960
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Db	961	GCCGATCAGCGGCTTTGAGGGCGGTTTTTTCGGGCGATACGAGAGAGCTTTCGGGCGG	1020
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Db	1021	TTTTATCAGTAACGACACAGCGTATTCGGCGTGTTCGACGGCAACAAAAACAGAGACA	1080
QY	1081	GCAACCGCATCAGATACAAATCTCTGCCCTTCGGAATAACACCAAAATCTTGGAT	1140
Db	1081	GCAACCGCATCAGATACAAATCTCTGCCCTTCGGAATAACACCAAAATCTTGGAT	1140
QY	1141	TCTCTAAAAATTTCCGTTGACGAGGGGACGTGATGACCATGCGCGTAAGTTTGCATTTCC	1200

Db	1141	TCTCTTAAAAATTTCCGTTTGACAGCGCTGATGACCATGCCCGTAAGTTTGCCATTTC	1200
Qy	1201	ACTATGCCCGATTTTGGTTCATCCCGACAAACTTCTTGTGGAAGGGCGTAAATTCCTTTC	1260
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Qy	1261	GTTAGCCCAAGAGAAAAACCATCGAGCTTCCCGACGGCAGGAAATGACCATCCGTGCTTGT	1320
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Qy	1381	CCGAAGCCGAGGATGAAGAGGATTCGGACATTTGATATGGCGAAGAAAGCGAAGACGAA	1440
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Qy	1441	ATTTCGAAGATGATTAACGGCGAAGATGAAGTCAACCGAAGAGAGAGAGCTGGAAGAAC	1500
Db	1441	ATTTCGAAGATGATTAACGGCGAAGATGAAGTCAACCGAAGAGAGAGAGCTGGAAGAAC	1500
Qy	1501	GAAGAAGAAACTGATGAAGACGAAGAGAGAAACCCGGAAGAAACTGGAAGAACTGAAGAA	1560
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Qy	1561	ACTGAAGAACTGAAGAACTGAAGAACTGAAGAAATCCCGACGACAGAGAGCGCAAC	1620
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Db	1621	GGCGGTTTCAGGACAGTCTTCCACCTCCGACCTCCGAGCCCTTAAAGCAGGACATCGACCTT	1680
Qy	1681	TTCTCTGAAAGGTATCCGACGCGGAGCCGACATTCGCGAAATTTGAAAAAGCAGCTAT	1740
Db	1681	TTCTCTGAAAGGTATCCGACGCGGAGCCGACATTCGCGAAATTTGAAAAAGCAGCTAT	1740
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LOCUS Neisseria meningitidis strain 881607 lactoferrin-binding protein
DEFINITION precursor (lbpB) gene, complete cds.
ACCESSION AF123383
VERSION AF123383.1 GI:4884692
KEYWORDS
SOURCE
ORGANISM Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 2124)
AUTHORS Pettersson, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tomassen, J.
TITLE Sequence variability of the Meningococcal lactoferrin-binding protein lbpB
JOURNAL Gene 231 (1-2), 105-110 (1999)
MEDLINE 99250255
PubMed 10231574
REFERENCE 2 (bases 1 to 2124)
AUTHORS Pettersson, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tomassen, J.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
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Query Match 72.0%; Score 1562.4; DB 1; Length 2124;
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Matches 1835; Conservative 0; Mismatches 286;

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LOCUS      A98976
DEFINITION Sequence 9 from Patent WO9909176.
ACCESSION A98976
VERSION   A98976.1
KEYWORDS   GI:6781936
SOURCE     Neisseria meningitidis
ORGANISM   Neisseria meningitidis
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            Neisseriaceae; Neisseria.

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REFERENCE
Petterson-Fernholm, A.M. and Tommassen, J.P.
NEISSERIA LACTOFERRIN BINDING PROTEIN
Patent: WO 9909176-A, 25-FEB-1999;
UNIV UTRECHT (NL); PETTERSSON FERNHOLM ANNIKA MAR (NL)

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ORIGIN

Query Match
Best Local Similarity 72.0%; Score 1562.4; DB 6; Length 2124;
Matches 1835; Conservativity 84.5%; Pred. No. 3.8e-313;
Mismatches 286; Indels 51; Gaps 5;

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RESULT 6

BD074759

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD074759 2124 bp DNA linear PAT 27-AUG-2002
Neisseria lactoferrin-binding protein.

BD074759

BD074759.1 GI:22620362

JP 2001514894-A/5.

unidentified

unclassified.

1 (bases 1 to 2124)

Felholm, A.M.P. and Thomsen, J.P.M.

Neisseria lactoferrin-binding protein

Patent: JP 2001514894-A 5 18-SEP-2001;

UNIVERSITY OF UTRECHT, TECHNOLOGY FOUNDATION

OS Unidentified

PN JP 2001514894-A/5

PD 18-SEP-2001

PF 10-AUG-1998 JP 2000509840

PR 15-AUG-1997 GB 9717423.9, 05-FEB-1998 GB 9802544.8 PI

ANICA MARGARETA PETERSON FELNHOLM, JOHANNES PETRUS MARIA PI

THOMSEN

PC C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22,

PC C07K16/12,

PC C12N1/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC

C12N15/00

CC Strandedness: Double;

CC Topology: Linear;

CC Neisseria lactoferrin-binding protein

PH Key Location/Qualifiers

FT source 1..2124

FT Location/Qualifiers

FEATURES

apparent

source

1. .2124

/organism="unidentified"
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ORIGIN

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Best Local Similarity 84.5%; Pred. No. 3.8e-313;
Matches 1835; Conservative 0; Mismatches 286; Indels 51; Gaps 5;
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DB 61 GCGGCAATTTTCGGCGTCAGCGCTTGTCTGCAATCAACGCCGACCGCGTACCCCGTCACT 120
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QY 181 GTCAACGACCGCGCTGCTGGGCAATGCGGCTTTCGACGCAATATTCGCACTTCT 240
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QY 241 CGTGAAGATGACCGCAATTTCCGATAGCAAAACGACGAGAAAGAACTGCTGTTAAA 300
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QY 481 GAGAAACATCGGATGAAAGCAAGTCTTCTAATCGTTTACGTTATGACGTTTGTATAT 540
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DB 541 TATTCGGGAGAACATCTCTCGCAATCTTTACGAGCGCGGAAACGTTGAAATATTCGGC 600
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DB 601 AACTGGCAATATATGACGATGCAATACGTCATCGGAGAGTTAA ---GGGGTTTCAGT 657
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QY 838 CCACTGACCATTTTCAACATTAACGCAACATTCGACGCAACCGCTTTTACCGCAGTGC 897
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QY 1378 AAACCGAAGCGCGAGGATGAGAGGATTCGCGACATTCATATATGCGAAGAGGAGCAAGAC 1437
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QY 1498 ACCGAGAGAAATCTGATGAAGACGAGAGGAGAACCCGAGAGAACTGGAAGAACTGAA 1557
DB 1482 --CGAGTCTGAGAGATGAGACGAGATGAGACGAGAGGAGGAGGAGGAGGAGGAGGAG 1533
QY 1558 GAACTGAAGAACTGAGAAACTGAGAAACTGAGAAACTGCGCGACAGAGAGAGGAGG 1617
DB 1534 GAACTTGAAGAGAGCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1593
QY 1618 AACGCGGTTTCAGCGAGCATCTTCGCGACCTTCGCGAGGAGGAGGAGGAGGAGGAGGAG 1677
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QY 1798 GGCACCTACGTCCTTCAAAAGGATAGCTATCGAATCAAGCGGCAAAACGAGAGATTGAC 1857
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DB 1873 GCTTTTATTTGAAAAAGGTGATGATGAGCAAGGTTTCCAGCTTTTGGCGGATCT 1932
QY 1978 CGTGAAAAATGAGTTGATTTGCTCGGCAAGGTTTCGACTAATCCCCCAAGTTTAAAGCC 2037
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/complement (1863. .1872)
/note="Core DNA uptake sequence: gcgctctgaa"
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/complement (1927. .2547)
/note="NMA1731"
/complement (1927. .2547)
/note="NMA1731"
206aa; similar to SW:P44013 (Y552_HAEIN) hypothetical protein from Haemophilus influenzae (207 aa) fasta scores; E(): 0, 59.6% identity in 203 aa overlap."
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/complement (2570. .2579)
/note="Core DNA uptake sequence: gcgctctgaa"
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/complement (2581. .3090)
/note="NMA1732"
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/note="NMA1732"
conserved hypothetical protein, len: 169aa; similar to SW:P43971 (Y243_HABIN) hypothetical protein from Haemophilus influenzae (172 aa) fasta scores; E(): 0, 49.7% identity in 169 aa overlap."
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membrane protein from Neisseria meningitidis (183 aa)
fasta scores; E(): 0, 96.7% identity in 183 aa overlap.
Contains Pfam match to entry PF00127 copper-bind, Copper
binding proteins, plastocyanin/azurin family and prosite
match to PS00196 Type-1 copper (blue) proteins signature."
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218.60, E-value 9.1e-62"
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preprotein translocase SecA subunit from Escherichia coli
(901 aa) fasta scores; E(): 0, 58.0% identity in 920 aa
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SecA protein, SecA protein, amino terminal region and
Prosite match to PS01312 Protein secA signatures."
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Best Local Similarity 67.0%; Score 1454.2; DB 1; Length 326301;
Matches 1742; Conservative 0; Mismatches 343; Indels 42; Gaps 4;

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18981 ATGTGTAACCGCAATATATGCGCGCATTTCTTGTTCCTTACTTTTGGCATCTTGCATC 18922
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18921 GCGCGCAATTTTCGGCGTGAGCCTGTGTTCGAATCAACGCCGCGGTACCCGCTCCT 18862
QY 121 TTCAAGTCTAAGGACGTTTCCACTTCGCCCTTCGCCGCTTCCTCGTAGAAGCAACGCCG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18861 TTCAAGTCTAAGGACGTTTCCACTTCGCCCTTCGCCGCTTCCTCGTAGAAGCAACGCCG 18802
QY 181 GTCAACGACCGCGCTTCGGTTCGGCAATCGCGCTTCGAGAGCGGATATCTGCTTTTCA 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18801 GTCAACGACCGCGCTTCGGTTCGGCAATCGCGCTTCGAGAGCGGATATCTGCTTTTCA 18742
QY 241 CGTGAAGATGGCAGCGCAATTCGGATAGCAACAAAGCAAGAGAGAAAGCTGCTGTTTAA 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18741 CGTGAAGATGGCAGCGCAATTCGGATAGCAACAAAGCAAGAGAGAAAGCTGCTGTTTAA 18682
QY 301 GAAGGTGATGTTCTGTTTATACCGTTCAGAGAAATTAACCTTCAACACTTAAAGC 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18681 GAAGGTGATGTTCTGTTTATACCGTTCAGAGAAATTAACCTTCAACACTTAAAGC 18622
QY 361 GAAATTCATAAAGCAATCTCGAGCAAGCATTTACCAATCGGAAATGAAGATTAAGAA 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18621 GAAATTCATAAAGCAATCTCGAGCAAGCATTTACCAATCGGAAATGAAGATTAAGAA 18562
QY 421 TATTAATTCGCTTGTTCAGTTCGGCTTATGTTTATCTAAACCGAAAGATGAAGAT 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18561 TATGTTTATGAATTTAGATGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 18502
QY 481 GAGAAACATCGGATGAAAGCAGTTTCTTAATCGTTTATGAGTTCAGTTCAGTTCAGTTC 540
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18501 GAGTGGACTTCAAAATCAACAGCTTTACCTACCGTTCAGTTCAGTTCAGTTCAGTTCAG 18442
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18441 TATCTCGAGAAACATCTTCCCAATCTTACCGAGCGCGGCAACGGTGAATATTCGGCG 18382
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18381 AACTGGCAATATATGACCGATGCCATAGCTATCGTAGAGAGGTAA--GGGGTTCAGT 18322
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18321 GAAGATTTGGTTCATACCATATATGTAAGTAATTCGGGAGCTTCCTATGAGGCT 18262
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18261 ACTGCGGACGACGAGGAGGAAACATCTCGCGGAATATACGGTTAA--TTTCGACAAAA 18202
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18201 AACTGGAGGTAAAGTTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCTTAAAT 18142
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18141 CCACTGACCATTTACCAATTCACGCAATTCGAGCGCAACCGCTTTACCGGAGTGC 18082
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18021 GATGCGGATCAGCGCTTGAGGCGGCTTTTTCGGCGATTAACGAGAGAGCTTCGCGG 17962
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RESULT 8
AF072890
LOCUS
DEFINITION
Neisseria gonorrhoeae lactoferrin binding protein B precursor
(lbpB) gene, complete cds.
AF072890
VERSION
KEYWORDS
AF072890.1 GI:4106392
SOURCE
ORGANISM
Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
1 (bases 1 to 2519)
Biswas,G.D., Anderson,J.E., Chen,C.J., Cornelissen,C.N. and
Sparling,P.F.
TITLE
Identification and functional characterization of the Neisseria
gonorrhoeae lbpB gene product
Infect. Immun. 67 (1), 455/459 (1999)
JOURNAL
MEDLINE
PUBMED
99081783
9864256
REFERENCE
AUTHORS
2 (bases 1 to 2519)
Biswas,G.D., Anderson,J.E., Cornelissen,C.N. and Sparling,P.F.
Direct Submission
TITLE
JOURNAL
SUBMITTED (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521
Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA
FEATURES
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/note="encodes gonococcal uptake sequence"

ORIGIN

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RESULT 9
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LOCUS
DEFINITION
Neisseria meningitidis strain H44/76 lactoferrin-binding protein precursor (lbpB) gene, complete cds.
ACCESSION
AF123380
VERSION
AF123380.1 GI:4884686
KEYWORDS
SOURCE
Neisseria meningitidis
ORGANISM
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 2226)
Pettersson, A., van der Biezen, J., Joosten, V., Hendriksen, J. and Tommaassen, J.
AUTHORS
Sequence variability of the meningococcal lactoferrin-binding protein lbpB
JOURNAL
Gene 231 105-110 (1999)
MEDLINE
99250255
PUBMED
10231574
REFERENCE
2 (bases 1 to 2226)
Pettersson, A., van der Biezen, J., Joosten, V., Hendriksen, J. and Tommaassen, J.
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (26-JAN-1999) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
FEATURES
Location/Qualifiers
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K"

Query Match 63.4%; Score 1375.8; DB 1; Length 2226;
Best Local Similarity 80.4%; Pred. No. 2e-274;
Matches 1710; Conservative 0; Mismatches 357; Indels 60; Gaps 6;
QY 1 ATGTGTAAACCGAATTATGGCGCATTTGCTTTGTTGCCCTTACTTTTGGCATCTTGTGATC 60
Db 1 ATGTGTAAACCGAATTATGGCGCATTTGCTTTGTTGCCCTTACTTTTGGCATCTTGTGAT 60
QY 61 GCGGCGCAATTCGGCGTGAGCTGTGTTCGATCAACCGCGACCGCGTACCCCGTCACT 120
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RESULT 10
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 VERSION A98972.1 GI:6781932
 KEYWORDS
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

REFERENCE
 AUTHORS Pettersson-Fernholm, A.M., and Tommassen, J.P.
 TITLE NEISSERIA LACTOFERRIN BINDING PROTEIN
 JOURNAL Patent: WO 9909176-A 5 25-FEB-1999;
 UNIV UTRECHT (NL); PETTERSSON FERNHOLM ANNIKA MAR (NL)
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ORIGIN

Query Match 63.4%; Score 1375.8; DB 6; Length 2226;
 Best Local Similarity 80.4%; Pred. No. 2e-274;
 Matches 1710; Conservative 0; Mismatches 357; Indels 60; Gaps 6;
 QY 1 ATGTGTAACCGAATATATGCGGCAATGCTTCTGTTGCCCTTACTTTTGGCATCTTGGATC 60
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Qy	1432	GAGAGCAATTTCCGAGATGATTAACGCGGAGATGATGATCACCAGAGAGGAGCT	1491
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Db	1870	CAACTGCTTTTCCATTTGAAACGCGGTGATTTGAGGCAATGATTCGCAAAATGATTC	1929
Qy	1972	CGTACTCGTCAAAATGCTTTGATTTCTCTGGGCAAGTTTCGACTAATCCCAAGTTT	2031
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Qy	2032	AAAGCCAGTAACTTCTGCTAGAGGAGGATTTTATGCTGCGAGGCGGAGTTGGGT	2091
Db	1990	AAAGCCAGTAACTTCTTGTAAACAGGCGCTTTTACGCGCGGAGGAGGATTTGGC	2049
Qy	2092	GGTAAATATTACGACAGTACCGGAA	2118
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RESULT 11

BD074757

LOCUS

BD074757

DEFINITION

Neisseria lactoferrin-binding protein.

ACCESSION

BD074757

VERSION

BD074757.1

GI:22620360

KEYWORDS

JP 2001514894-A/3.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 2226)

AUTHORS

Felnholm, A.M.P. and Thomassen, J.P.M.

TITLE

Neisseria lactoferrin-binding protein

JOURNAL

Patent: JP 2001514894-A 3 18-SEP-2001;

UNIVERSITY OF UTRICHT, TECHNOLOGY FOUNDATION

COMMENT

OS Unidentified

PN JP 2001514894-A/3

PD 18-SEP-2001

PF 10-AUG-1998

PI 2000509840

PR 15-AUG-1997

GB 9717423.9

05-FEB-1998

GB 9802544.8

PI

ANICA MARGARETA PETERSON FELNHOLM, JOHANNES PETRUS MARIA

THOMASSEN

PC C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22,

C07K16/12,

PC C12N1/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC

C12N15/00

CC Strandedness: Double;

CC topology: Linear;

CC Neisseria lactoferrin-binding protein

FF Key

FF Location/Qualifiers

FT source

1. .2226

/organism='Unidentified'.

FT Location/Qualifiers

1. .2226

/organism='unidentified'

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Best Local Similarity		80.4%; Pred. No. 2e-274;	
Matches 1710; Conservative		0; Mismatches 357; Indels 60; Gaps 6;	
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AE002504/c

LOCUS

DEFINITION

Neisseria meningitidis serogroup B strain MC58 section 146 of 206

of the complete genome.

ACCESSION

AE002504 AE002098

VERSION

AE002504.1 GI:7226785

KEYWORDS

SOURCE

Neisseria meningitidis MC58

ORGANISM

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria.

REFERENCE

AUTHORS

1 (bases 1 to 9955)

Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,

Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,

Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,

Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,

Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,

Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,

Pizza, M., Grandi, G., Sun, L., Scarlato, V., Massignani, V.,

Rappuoli, R. and Venter, J.C.

Complete genome sequence of Neisseria meningitidis serogroup B

strain MC58

Science 287 (5459), 1809-1815 (2000)

20175755

10710307

2 (bases 1 to 9955)

Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,

Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,

Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,

Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,

Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,

Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,

Pizza, M., Grandi, G., Sun, L., Scarlato, V., Massignani, V.,

Rappuoli, R. and Venter, J.C.

Direct Submission

Submitted (17-MAR-2000) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

FEATURES

Location/Qualifiers

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Qy	1966	TTGGCGGTACTCGTGAATAAGTGTGATTGTCTGGCAAGTTCGACTAATCCCAAA	2025
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ORGANISM	Neisseria meningitidis		
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AUTHORS	Neisseriaceae; Neisseria.		
	1		
	Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J.C.,		
	Masignani, V., Galeotti, C., Moxa, M., Ratti, G., Scarselli, M.,		
	Scarlato, V., Rappuoli, R., Frazer, C.M. and Grandi, G.		
TITLE	Neisseria genomic sequences and methods of their use		
JOURNAL	Patent: WO 0066791-A 112 09-NOV-2000;		
FEATURES	CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)		
	Location/Qualifiers		

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ORIGIN

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QY	301	GAAGTGATGTCGTGTTTATACGTTTCAAGAAATAAATCTCAACAACTTAAAGC 360
Db	400	GAAGTGATGTCGTGTTTATACGTTTCAAGAAATAAATCTCAACAACTTAAAGC 459
QY	361	GAAATTCATAACGTAATCTCGAGGCAAGCATACCATCGGAAATGAAATATAAAAA 420
Db	460	GAAATTCATAACGTAATCTCGATGTAGAAATAGGACATCAGAAAGGAAATATAAAAA 519
QY	421	TATAATTCAGGTTGTGTCAGTCCGGTTATGTTGTTTACTAAACCGGAAAGATGAAAT 480
Db	520	TATGATTTAAATTTGTAGATGTCAGTTTATGAT ---ATGTAAGGGGAAAGATGAAAT 576
QY	481	GAGAAACATCGGATGAAGACGTTTCTAATCGTTTAGGTATGACGTTTCTGATAT 540
Db	577	AAGTGACCTTCAGATTACAAGCAGTTTCCACCGCTTAGGTATGACGTTTCTGATAT 636
QY	541	TATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGAAACGTTGAAATATTCGGC 600
Db	637	TATTCGGAGAACGTCCTTCCCAATCTTTACCGAGTGGGNAACGTTGGAATATCTGGT 696
QY	601	AACCTGGCAATATACCGGATGCCATAGCTCATCGGAGAGGTAAAGGGGTTTCCAGTGTG 660
Db	697	AACTGGCAATATACCGGATGCCAAAGCTCATCGAGCAGGTAAGCGGTTTGGCATTCAC 756
QY	661	GAATTTGGTATACACATATATGTAATGTAATGTAATTTGGGCGAGCTTCTTATGAGCTAG 720
Db	757	AAATTTGGGTTATACATTTTATGTAACGATGTTGGTGAACCTTCTTATCGGCTTAG 816
QY	721	GATGCGATGGCGGGGAAAAACATCTGCGCAATATACGTTTAAATTTGACAAAAAAAC 780
Db	817	GATGTCGAGAAAGGAAAAACATCTGCTAATATATACGTTAGATTCGGTAAACAAAC 876
QY	781	CTGGAAGGTAAAGTTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCCTTAAATCCA 840
Db	877	CTGACGGCGAGCTGATTAATAAACCAATATGTCAAACCCAGTGAGAAGC ---AAAAACCG 933
QY	841	CTGACCATTTACAAATTAACGCAATTTGGAGCGCAACCGCTTTTACCGGCGAGTGCCAAA 900
Db	934	CTGACCATTTACAAATTAACCTGCGGATTTAAACCGCAACCGCTTTTACCGGCGAGTGCCA 993
QY	901	GTTAGCACCGGAGTGAAGACGCAACGCTGATAAAGATAATTTGTTTTCATACCGAT 960

Db	994	GTCAATCTCTGATTTAGCGAAAAAGCCATGCAATAAGAGCATTTGTTTTCCATCGCGAT 1053
QY	961	GCCGATCAGCGGCTTGAGGCGGTTTTTTTCGGCGATAACGAGAGAGCTTTCGCGGCGG 1020
Db	1054	GCCGATCAGCGGCTTGAGGCGGTTTTTTTCGGCGATAAGGGGGAAGAGCTTTCGCGGACG 1113
QY	1021	TTTTATCAGTAACGACAAACAGCGTATTCGGCGTGTTCGAGGCAACAAAAACAGAGACA 1080
Db	1114	TTTTATCAGTAACGACAAACAGCGTATTCGGTGTATTCGAGGCAACAAAAATAGCC --- 1168
QY	1081	GCAACGCATCAGATACAAATCTCTGCTGCTGCGTCTGGAATAACACACCAAAATCTTGAT 1140
Db	1169	-----CCGTGCGCTCTGGAATAACACACCAAAATCTTGAT 1203
QY	1141	TCTCTAAATAATTCGTTGAGGCGGACATGATGACCATGCCCTAAGTTTGGCATTTCC 1200
Db	1204	TCTCTGAAATAATTCGTTGATGAGGCAAGTGTGAAATCCCCGACCGTTTGGCATTTCT 1263
QY	1201	ACTATGCCCGATTTTGGTTCATCCCGACAAATCTTCTGTGGAAGCGGCGTGAATTCCTTTG 1260
Db	1264	CTATGCCCGATTTTGGTTCATCCCGACAAATCTTCTGTGGAAGCGGCGTGAATTCCTTTG 1323
QY	1261	GTTAGCCAGAGAAAAACATTCGAGCTTTCGCGACGCGAGAAATGACCATCGTGTCTGT 1320
Db	1324	GTTAGCCAGAGAAAAACATTCGAGCTTTCGCGACGCGAGAAATGACCATCGTGTCTGT 1383
QY	1321	TGCGATTTCTGACCTATGTGAATCTCGGACGATATAAACCGACCGCGCGCTCAAA 1380
Db	1384	TGCGACTTTTTGACCTATGTGAATCTCGGACGATATAAACCGACCGCGCGCTCAAA 1443
QY	1381	CCGAGGCGCAGGATGAAGAGATTCGACATTTGATATGCGGAAGAAAGCGAAGCAAA 1440
Db	1444	CCGAGGCGCAGGACGAGAGATTCGACATTTGATATGCGGAAGAAAGCGAAGCAAA 1503
QY	1441	ATTTCCGAGATGATATACGCGAAGATGAACTCCGAGAGAGAGAGAGAGCTGAAAGAAC 1500
Db	1504	ATCGCGATGTAAGAGAGGACCGAGATGACCGCGAGAGATGAAAGCGGACGAGAA 1563
QY	1501	GAAGAGAAACTGTATGAAGACGAGAGAGAAACCGGAGAAACTGTAAGAACTGAAGAA 1560
Db	1564	GACGAAGCCACAGAAACGAGACGCGGAGAA --- 1596
QY	1561	ACTGAAGAAACTGAAGAAACTGAAGAAACTGAAGAAACTGAAGAAACTGAAGAAACT 1620
Db	1597	-----GACGAAGCTGAAGAACTGAAGAAACTGAAGAAACTGAAGAACTGAAGAA 1641
QY	1621	GCGGTTTCAAGGAGATCTCTGCGCACTCCGGAAGCTCTTAAGCGGAGGACATCGACCT 1680
Db	1642	GCGAGTTCAAAACGCGCATCTGCTGTCCGGAAGCTCTTAAGCGGAGGATATCGACCT 1701
QY	1681	TTCTGTAAGGTATCCGACGCGGAGCGGACATTCGCAAAATTCGCAAAATTCGCAAAATTCGCAAA 1740
Db	1702	TTCTGTAAGGTATCCGACGCGGAGAGATATTCGCAAACTGGAAGAGCAAGCTAT 1761
QY	1741	ACCGGCTCTGGAAGCGGCTATCGGCTGCGGATAGAAAGAGCGGAAACAGTATGATGCG 1800
Db	1762	ACCGGCTCTGGAAGCGGCTATCGGCAACCCATTCATGGAACATCATCGCGAT --- 1818
QY	1801	ACTAGTCCATCAAAAGGATGCTATCGGATCAAGCGGCAAAAGAGATTTGACGTT 1860
Db	1819	-----AAAGAGCGGCAAAAGAGATTTTACCGTT 1848
QY	1861	GATTTTGTGGAAGTCTGCTTTTACGTTAAGTTGACAGAAAAAATGATACACACCCCGCT 1920
Db	1849	GATTTTGTGGAAGATTCGATTTCCGGAACGCTGACGAGAAAAACGTTAGAACCTGCT 1908
QY	1921	TTTTATTTGAAAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db	1909	TTCCGTTATGAAAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1968
QY	1981	GAAATGTTGTTGATTTGTTCTGCGCAAGCTTCGATTAATCCCAAGTTTTTAAAGCGAT 2040

Search completed: August 24, 2004, 23:47:12
Job time : 8152.32 secs

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:48:44 ; Search time 734.857 Seconds
(without alignments)
12538.967 Million cell updates/sec

Title: US-10-735-098-3
Perfect score: 2169
Sequence: 1 atgtgtaaacgaattatgg.....tcgaggagggtggaataatga 2169

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq 29Jan04.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001s.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002s.*
- 7: geneseqn2003s.*
- 8: geneseqn2003bs.*
- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2169	100.0	2169	2	Aax23320 N. mening
2	1562.4	72.0	2124	2	Aax23323 N. mening
3	1454.2	67.0	2226	7	Aca41945 Prokaryot
4	1375.8	63.4	2226	2	Aax23321 N. mening
c 5	1360.8	62.7	110000	3	Continuation (2 of
c 6	1360.8	62.7	349980	3	Aaf21611 Neisseria
7	1304.8	60.2	2277	2	Aax23319 N. mening
8	1250.6	57.7	2262	2	Aax23322 N. mening
c 9	868.2	40.0	14652	3	Aaa81482 N. mening
10	491.6	22.7	707	3	Aaa81815 N. mening
11	439.2	20.2	1000	4	Aaf91389 N. mening
12	439.2	20.2	1000	6	Abk37769 DNA seque
13	94.6	4.4	400	5	Aas75460 DNA encod
14	94.6	4.4	963	5	Aas68580 DNA encod
c 15	94	4.3	453	5	Aas92079 DNA encod
16	94	4.3	708	5	Aas69547 DNA encod
17	94	4.3	708	5	Aas75461 DNA encod
18	92.8	4.3	1686	2	Aaq87587 DNA encod
19	92.8	4.3	29392	2	AAV15422 Mouse pol
20	92	4.2	2334	5	Aas90705 DNA encod
c 21	90.6	4.2	496	4	Aai12609 Probe #25
c 22	90.6	4.2	496	4	AbA54309 Human foe
c 23	90.6	4.2	496	4	Aai33960 Probe #26

c 24	90.6	4.2	496	4	ABA43847	AbA43847 Human bre
c 25	90.6	4.2	496	4	ABA24068	AbA24068 Probe #25
c 26	90.6	4.2	496	4	AAK28026	Human bon
c 27	90.6	4.2	496	4	AAK02592	Human bra
c 28	90.6	4.2	496	4	ABS27626	Human liv
c 29	90.6	4.2	496	5	AAI02512	Probe #25
c 30	90.6	4.2	496	6	ABS02506	Human gen
c 31	89.8	4.1	248	5	AAAG90707	DNA encod
c 32	89.8	4.1	305	4	AAI21797	Probe #11
c 33	89.8	4.1	305	4	ABA66871	Human foe
c 34	89.8	4.1	305	4	AAI47083	Probe #15
c 35	89.8	4.1	305	4	ABA48950	Human bre
c 36	89.8	4.1	305	4	ABA33942	Probe #12
c 37	89.8	4.1	305	4	AAK41027	Human bra
c 38	89.8	4.1	305	4	AAK15306	Human bra
c 39	89.8	4.1	305	4	ABS40624	Human liv
c 40	89.8	4.1	305	5	AAI07480	Probe #74
c 41	89.8	4.1	305	6	ABS15007	Human gen
c 42	89.8	4.1	483	5	AAS69549	DNA encod
c 43	89.6	4.1	276	4	AAI23164	Probe #13
c 44	89.6	4.1	276	4	ABA68266	Human foe
c 45	89.6	4.1	276	4	ABA35275	Probe #13

ALIGNMENTS

RESULT 1
AAX233320
ID AAX233320 standard; cDNA; 2169 BP.
XX
AC AAX233320;
XX
DT 11-JUN-1999 (first entry)
XX
DE N. meningitidis strain M981 LbpB cDNA.

LbpB; lactoferrin binding protein; vaccine; neisserial disease; meningitis; diagnosis; treatment; ds.
XX
OS Neisseria meningitidis.

Key Location/Qualifiers
CDS 1..2169
FT /*tag= a
FT /product= "LbpB"

PN WO9909176-A1.

PD 25-FEB-1999.

PF 10-AUG-1998; 98WO-EP005117.

PR 15-AUG-1997; 97GB-00017423.

PR 05-FEB-1998; 98GB-00002544.

PA (UYUT-) RIJKSUNIV UTRECHT.

PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.

PI Pettersson-Fernholm AM, Tommassen JPM;

PI WPI; 1999-190165/16.

DR P-FSDB; AAW93493.

XX New lactoferrin-binding protein B polynucleotides - obtained from

Neisseria meningitidis, used to develop products for the diagnosis, prevention and treatment of neisserial disease, e.g. meningitis.

XX Claim 2; Page 82-86; 116pp; English.

XX This invention describes novel lactoferrin-binding protein B (lbpB) strains of Neisseria meningitidis. The products of this invention can be used for vaccinating humans against neisserial disease e.g. meningitis.

CC Antibodies raised against the proteins of the invention can be used for
CC diagnosing or treating neisserial disease in humans. The LbpB
CC polypeptides can also be used for identifying compounds which inhibit the
CC polypeptides

AX	SQ	Sequence	2169 BP; 675 A; 457 C; 550 G; 487 T; 0 U; 0 Other;
		Query Match	100.0%; Score 2169; DB 2; Length 2169;
		Best Local Similarity	100.0%; Pred. No. 0;
		Matches 2169; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGTTGTAACCGCAATATGGCGGCATCTCTTGTTGCCCTTACTTTTGGCATCTTGCATC	60
DB	1		60
QY	61	GGCGGCAATTTTCGGCGTGCACCTGTTTTCGAATCAACGCCGACCGGTATACCCGTCAC	120
DB	61	GGCGGCAATTTTCGGCGTGCACCTGTTTTCGAATCAACGCCGACCGGTATACCCGTCAC	120
QY	121	TTCAAGTCTAAGGAGGTCCACATTCGCCCCCTCCGGTCTTCGGTAGAACAACACGCGG	180
DB	121	TTCAAGTCTAAGGAGGTTCACATTCGCCCCCTCCGGTCTTCGGTAGAACAACACGCGG	180
QY	181	GTCACACAGCCCGCGTCGGTTCGGCAATGCGGTGTTTGAGACGGAATPACTGCTTTTCAT	240
DB	181	GTCACACAGCCCGCGTCGGTTCGGCAATGCGGTGTTTGAGACGGAATPACTGCTTTTCAT	240
QY	241	CGTGAAGATGGCAGCGCAATTCCTCGATAGCAAAACGACAGAGAAAGCTGCTTTTAAA	300
DB	241	CGTGAAGATGGCAGCGCAATTCCTCGATAGCAAAACGACAGAGAAAGCTGCTTTTAAA	300
QY	301	GAAAGTGATGTTCTGTTTTTATACGGTTCAAAAGAAAAATAAATCTCAACAACCTAAAAAGC	360
DB	301	GAAAGTGATGTTCTGTTTTTATACGGTTCAAAAGAAAAATAAATCTCAACAACCTAAAAAGC	360
QY	361	GAAATTTCAATAACGTAATCTCTGAGGCAAGCATTCACCATCGGAAATGAAATAAAAA	420
DB	361	GAAATTTCAATAACGTAATCTCTGAGGCAAGCATTCACCATCGGAAATGAAATAAAAA	420
QY	421	TATAATATCGGTTTGTTCAGTCCGGTTATGTTTACTTAAAAACGGAAGATGAAAT	480
DB	421	TATAATATCGGTTTGTTCAGTCCGGTTATGTTTACTTAAAAACGGAAGATGAAAT	480
QY	481	GAGAAAAATCGGATGAAAAAGCAGTTTTCTTAATCGTTTAGGCTATGACGGTTTTGTATAT	540
DB	481	GAGAAAAATCGGATGAAAAAGCAGTTTTCTTAATCGTTTAGGCTATGACGGTTTTGTATAT	540
QY	541	TATCTCGGAGAACATCTCTTCCCAATCTTTACCGAGCGGGAAACGGTGAATATTCCCGC	600
DB	541	TATCTCGGAGAACATCTCTTCCCAATCTTTACCGAGCGGGAAACGGTGAATATTCCCGC	600
QY	601	AACTGGCAATATAGACCGATGCCATACGTCAATCGGAGAGGTAAAGGGGTTTCCAGTGTG	660
DB	601	AACTGGCAATATAGACCGATGCCATACGTCAATCGGAGAGGTAAAGGGGTTTCCAGTGTG	660
QY	661	GATTTGGGTTATACCAATATTTATGGTAATGAAATTTGGGGCAGCTTCTTATGAGGCTAGG	720
DB	661	GATTTGGGTTATACCAATATTTATGGTAATGAAATTTGGGGCAGCTTCTTATGAGGCTAGG	720
QY	721	GATGCCGATGGCGGAAAAACATCTCGCGCAATATACGTTTAAATTCGCACAAAAAACAAC	780
DB	721	GATGCCGATGGCGGAAAAACATCTCGCGCAATATACGTTTAAATTCGCACAAAAAACAAC	780
QY	781	CTGGAGGTAAAGTTGATTAATAAATCAGTATGTGCAAAAGAGAGATGATCTCTAAAAATCCA	840
DB	781	CTGGAGGTAAAGTTGATTAATAAATCAGTATGTGCAAAAGAGAGATGATCTCTAAAAATCCA	840
QY	841	CTGACCATTTACAAATATACCGCAACATTTGGACGGCAACCGCTTTTACCGCAGTGCCAAA	900
DB	841	CTGACCATTTACAAATATACCGCAACATTTGGACGGCAACCGCTTTTACCGCAGTGCCAAA	900
QY	901	GTTTAGCACCGAGGTGAAGACGCAACACGCTGATTAAGAAATATTGTTTTTCCATACCGAT	960

QY 2041 AATCTTCTGTAGAGGAGATTATATGTCGCGAGGCGGACAGAGTTGGGTGGTAATATT 2100
 Db |||||
 QY 2041 AATCTTCTGTAGAGGAGATTATATGTCGCGAGGCGGACAGAGTTGGGTGGTAATATT 2100
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 QY 2101 ATCGACAGTACCGGAAATCGCGTGGTATTTCGGTGGGAGAAAGATATGACGAGGTG 2160
 Db |||||
 QY 2101 ATCGACAGTACCGGAAATCGCGTGGTATTTCGGTGGGAGAAAGATATGACGAGGTG 2160
 Db |||||
 QY 2161 GAAATATGA 2169
 Db |||||
 QY 2161 GAAATATGA 2169
 Db |||||

RESULT 2
 AAX23323
 ID AAX23323 standard; cDNA; 2124 BP.

AC AAX23323;

DT 11-JUN-1999 (first entry)

XX N. meningitidis strain 881607 LbpB cDNA.

XX LbpB; lactoferrin binding protein; vaccine; neisserial disease;
 KW meningitis; diagnosis; treatment; ds.

XX Neisseria meningitidis.

XX Key Location/Qualifiers
 FH 1. -2124
 FT /*tag= a
 FT /product= "LbpB"

XX WO9909176-A1.

XX 25-FEB-1999.

XX 10-AUG-1998; 98WO-EP005117.

XX 15-AUG-1997; 97GB-00017423.

XX 05-FEB-1998; 98GB-00002544.

XX (UK)- RIJKSUNIV UPRECHT.

XX (TECH-) TECHNOLOGY FOUND TECHNOLOGIEBIOTICHTING ST.

XX Pettersson-Fernholm AM, Tommassen JPM;

XX WPI; 1999-190165/16.

XX P-PSDB; AAW93496.

XX New lactoferrin-binding protein B polynucleotides - obtained from
 PT Neisseria meningitidis, used to develop products for the diagnosis,
 PT prevention and treatment of neisserial disease, e.g. meningitis.

XX Claim 2; Page 105-109; 116pp; English.

XX This invention describes novel lactoferrin-binding protein B (LbpB)
 CC strains of Neisseria meningitidis. The products of this invention can be
 CC used for vaccinating humans against neisserial disease e.g. meningitis.
 CC Antibodies raised against the proteins of the invention can be used for
 CC diagnosing or treating neisserial disease in humans. The LbpB
 CC polypeptides can also be used for identifying compounds which inhibit the

XX Sequence 2124 BP; 663 A; 461 C; 541 G; 459 T; 0 U; 0 Other;

XX Query Match 72.0%; Score 1562.4; DB 2; Length 2124;

XX Best Local Similarity 84.5%; Fred. No. 0;

XX Matches 1835; Conservative 0; Mismatches 286; Indels 51; Gaps 5;

QY 1 ATGTGTAACCGAATTATGCGGCAATTCCTGTTGCGCTTACTTTGGCATCTTGATC 60
 |||||

Db |||||
 QY 1 ATGTGTAACCGAATTATGCGGCAATTCCTGTTGCGCTTACTTTGGCATCTTGATC 60
 QY 61 GCGGCAATTTCCGGCTGCAGCCTGTTGTCGAATCAAGCCGACCGCTACCCCGTCACT 120
 Db |||||
 QY 61 GCGGCAATTTCCGGCTGCAGCCTGTTGTCGAATCAAGCCGACCGCTACCCCGTCACT 120
 QY 121 TTCAAGTCTAAGAGAGTTCCCACTTCGCCCTGCGGGTCTTCGGTGAACCAACGCG 180
 Db |||||
 QY 121 TTCAAGTCTAAGAGAGTTCCCACTTCGCCCTGCGGGTCTTCGGTGAACCAACGCG 180
 QY 181 GTCACACGCGCGCTGCGGCAATTCGCCCTGCGGGTCTTCGGTGAACCAACGCG 240
 Db |||||
 QY 181 GTCACACGCGCGCTGCGGCAATTCGCCCTGCGGGTCTTCGGTGAACCAACGCG 240
 QY 241 CGTGAAGATGCGACGCGCAATTCGCCCTGCGGGTCTTCGGTGAACCAACGCG 300
 Db |||||
 QY 241 GATAAGGATGCAATGATTTTCCAAATAGCAACACGAGAGAAAGCTGTCGTTTAAA 300
 QY 301 GAAGTGATGTTCTGTTTATAGCGTTCAAAAGAAATAAATCTTCAACACTTAAAGC 360
 Db |||||
 QY 301 GAGGAAGATATCTCTGTTTATACGTTTCCAAAGATCAACGTCAGCAGCTTAAAGAT 360
 QY 361 GAATTCATTAACGTTAATCCTGAGCGACGATTACCATCGAAATCGAAATTAATAA 420
 Db |||||
 QY 361 AAAATTCGTCAACCAATCTTACGCGCAAGCATTACCATCGAAATTAATAA 420
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 QY 481 GAGAAACATCGATGAAAGAGAGTTTCTAATCGTTTATGAGCTATGACGTTTGTATAT 540
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 QY 541 TATTCGGAGAACATCTTCCCAATCTTACCGGCGGCGGCAACGTTCAATATTCGCGC 600
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 QY 601 AACTGGCAATATATGACCGATGCCATAGCTCATCGGAGAGAGCTAA--GGGCTTCCAGT 657
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 Db |||||
 QY 658 GTGATTTGGGTTATATCGTTTATGCGTCAAAATGTCGAGCAACTCTTATGCTGCG 720
 QY 718 AGGATCGGATGCGCGGAAACATCTTCCCAATATGCGGCAATATGCGTAAATTCGACAA 777
 Db |||||
 QY 721 ACTGCCAGCACCGGAGGAGAAACATCTTCCCAATATGCGGCAATATGCGTAAATTCGACAA 780
 QY 778 AACTGGAGGTAAGTTGATTAAATCAGTATGTCAAAGAGAGATGATCCTTAAATAT 837
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 QY 781 ACTCTGAATGCAAGCTGATTAATAATCAGTATGTCGCAAGAGAGATGATCCTTAAATA 840
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 Db |||||
 QY 841 CCATGACCATTTACCGCAATTTACTGCAAAATTTGAGCGCAACCGCTTACCGGAGTCC 900
 QY 898 AAAGTTAGCCAGGTTGAGAGCGACACGCTGATTAAGATATTTGTTTTCATACC 957
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 QY 901 AAAGTTAGCCAGGTTGAGAGCGAATCAGCTGATTAAGATATTTGTTTTCATACC 960
 QY 958 GATGCCGATCAGCGCTTGGGCGGTTTTCGCGGATTAACGAGAGAGTTCGCCGG 1017
 Db |||||
 QY 961 GATGCCGATCAGCGCTTGGGCGGTTTTCGCGGATTAAGGAGAGTTCGCCGG 1020
 QY 1018 CGGTTTATCAGTAACGACACAGCGTATTCGGGTTTCGCGGCAACCAACCAACAGAG 1077
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 QY 1021 CGGTTTATCAGTAACGACACAGCGTATTCGGGTTTCGCGGCAACCAACCAACAGAG 1080
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 QY 1081 ACAGCAACGATCAGATCAATCTGCGCTCGGCTCGGAAACACACCAACCAATCTTG 1140

QY 1138 GATTCTCTAAAAATTTCCGTTGACGAGCGGACTGATGACCATGCCCGTAAGTTTCCCATTT 1197
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 Db 1381 CAACCGAAGGCGCAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
 QY 1438 GAAATTCGGAAGATGATTAACGCGAAGATGAGTCAACGGAAGAGAGAGAGAGAGAGAG 1497
 Db 1441 GAAA---GCGAAGACGAATTCGCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1481
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 Db 1482 ---CGAAGTCGTAAGAGATGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1533
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 Db 1534 GAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAG 1593
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 QY 1738 TATACCGGCACTTGGAAGGCGGTATCGCGGTGCGGATGAGAGAGAGAGAGAGAGAG 1797
 Db 1714 TATACCGGCACTTGGAAGGCGGTATCGCGGTGCGGATGAGAGAGAGAGAGAGAGAG 1753
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 QY 1858 GTTGATTTTGGTGGAGAGTGGCTTTCAGTGAAGTTCAGAGAGAGAGAGAGAGAGAG 1917
 Db 1813 GTTGATTTTGGTGGAGAGTGGCTTTCAGTGAAGTTCAGAGAGAGAGAGAGAGAGAG 1872
 QY 1918 GCTTTTATATGAAAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1977
 Db 1873 GCTTTTATATGAAAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1932
 QY 1978 CGTGAATATGTTGATTTGTTCTGGGAGAGTTCGACTAATCCCAAGTTTAAAGCC 2037
 Db 1933 CCGGAGAGAGGATTTGACCTTTCTGGGAGAGTTCGACTAATCCCAAGTTTAAAGCC 1992
 QY 2038 AGTAATCTTCTGTAAGAGAGATTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2097
 Db 1993 GCAATCTTCTGTAAGAGAGATTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2052
 QY 2098 ATTATCGAGTGAACGGAATTCGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2157
 Db 2053 ATTATCGAGTGAACGGAATTCGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2112
 QY 2158 GTGGAATATGA 2169
 Db 2113 GCAACAGATGA 2124

RESULT 3
 AC41945
 ID AC41945 standard; DNA; 2226 BP.
 XX ACA41945;
 AC ACA41945;
 DT 19-JUN-2003 (first entry)
 XX
 DE Prokaryotic essential gene #23602.
 XX
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 drug design; gene.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI: 2003-029926/02.
 DR P-PSDB; ABU38075.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 29815; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 the 6213 antisense sequences given in the specification where expression
 of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway
 required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 pathway in which a proliferation-required gene or its gene product lies
 or a gene on which the test compound that inhibits proliferation of an
 organism acts; (9) manufacturing an antibiotic; (10) profiling a
 compound's activity; (11) a culture comprising strains in which the gene
 product is overexpressed or underexpressed; (12) determining the extent
 to which each of the strains is present in a culture or collection of
 strains; or (13) identifying the target of a compound that inhibits the
 proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 for cellular proliferation to isolate candidate molecules for rational
 drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences


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QY 1252 ATTCTTTGGTTAGCCAGAGAAACCATCGAGCTTCCGCGCGGAGGAAATGACCATC 1311
DB 1258 ATTCTTTGGTTAGCCAGAGAAACCATCGAGCTTCCGCGCGGAGGAAATGACCGTC 1317
QY 1312 CGTCTTTGGTTAGCCAGAGAAACCATCGAGCTTCCGCGCGGAGGAAATGACCATC 1371
DB 1318 CGTCTTTGGTTAGCCAGAGAAACCATCGAGCTTCCGCGCGGAGGAAATGACCGCCA 1377
QY 1372 GCCGTCAAAACCGAGGCGCAGGATGAAGAGATTGGGACATTTGATTAATGGCGAAGAACG 1431
DB 1378 GCAAGTAAACCAAAGGCGGAGAGTAAAGGAGGATGAAGAGGATACAGGCGTTGGTAAC 1437
QY 1432 GAAGACGAATTTCCGAGAGATGAACCGCGAAGATGAAGTACCGAAGAGAGAGAGCT 1491
DB 1438 GACGAAGAGGACCGGAGATGAAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1497
QY 1492 GAAGAAACCGAAGAGAACTGATGAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1551
DB 1498 GGCBA---TGAAGAGAGGAGTGGAGAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGG 1554
QY 1552 ACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA 1611
DB 1555 -----GACGAAGCTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA 1602
QY 1612 GAAGCGAACGCGGTTGAGGAGGATCTGCGGATCTGCGGAGGAGGAGGAGGAGGAGGAG 1671
DB 1603 GCGCGCGGTTGAGGAGGATCTGCGGATCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1662
QY 1672 ATCGACCTTTTCTGGAAGGATCCGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1731
DB 1663 ATCGACCTTTTCTGGAAGGATCCGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1722
QY 1732 GCACGCTATACCGGCTATGGAAGCGGATCGCGGATCGCGGATCGCGGATCGCGGATCG 1791
DB 1723 GCACGCTATACCGGCTATGGAAGCGGATCGCGGATCGCGGATCGCGGATCGCGGATCG 1782
QY 1792 CTAGATGGCACTAGTCCATTCAGAGGATGAGTATGCGGATGAGGAGGAGGAGGAGGAG 1851
DB 1783 GCGGAT-----AAAAAGCGGCAAAAGCAGAA 1809
QY 1852 TTTCAGCTTGATTTTGGTGGAGTCCGCTTTGAGTGAAGTGAAGAGGAGGAGGAGGAGGAG 1911
DB 1810 TTTCAGCTTGATTTGCGGAGGAGTGAAGTTCGCGAGCTGAGCGGAGGAGGAGGAGGAG 1869
QY 1912 CACCCCGCTTTTATATGGAAGAGGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1971
DB 1870 CAACCTGCTTTCCATATGGAAGCGGCTGATTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1929
QY 1972 GGTACTCGTGAAGTGTGATTTGTTGGGCAAGTTCGACTAATCCCAAGTTT 2031
DB 1930 CGCACTCGGAGTACCGGATCAATCTTTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1989
QY 2032 AAAGCCAGTAACTTCTCGTAGAGGAGGATTTTATGTCGCGAGGAGGAGGAGGAGGAGGAG 2091
DB 1990 AAAGCCAGTAACTTCTTGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2049
QY 2092 GGTAAATATTCGACAGTACCGGAAA 2118
DB 2050 GGTACTATTTCAATAATGAGGAAA 2076
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RESULT 5
AAA81489_1/c
Continuation (2 of 9) of AAA81489 from base 100001 (N. meningitidis partial DNA sequence)
WP Sequence split into 9 fragments LOCUS AAA81489 Accession AAA81489
WP Fragment Name Begin End
WP AAA81489_0 1 110000
WP AAA81489_1 100001 210000
WP AAA81489_2 200001 310000
WP AAA81489_3 300001 410000
WP AAA81489_4 400001 510000
WP AAA81489_5 500001 610000
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WP AAA81489_6 600001 710000
WP AAA81489_7 700001 810000
WP AAA81489_8 800001 837096

Query Match 62.7%; Score 1360.8; DB 3; Length 110000;
Best Local Similarity 79.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 367; Indels 90; Gaps 5;

QY 1 ATGTGTAACCGAATTTATGGCGCAATTTGTCTGTGTTGCCCTTACTTTTGGCATCTTGATC 60
DB 64252 ATGTGTAACCGAATTTATGGCGCAATTTGTCTGTGTTGCCCTTACTTTTGGCATCTTGATC 64193
QY 61 GGCGGCAATTTTCGGCGTGGAGCTTGTCTGAAATCAAGCGCGCATCCCGTCACT 120
DB 64192 GGCGGCAATTTTCGGCGTGGAGCTTGTCTGAAATCAAGCGCGCATCCCGTCACT 64133
QY 121 TTCAAGTCTAAGGAGCTTCCCACTTCGCCCTTCGGGTCTTGGTAGAAGCAACCGCG 180
DB 64132 TTCAAGTCTAAGGAGCTTCCCACTTCGCCCTTCGGGTCTTGGTAGAAGCAACCGCG 64073
QY 181 GTCAACCGAGCGCGCTCGGTGCGCAATGCGGCTGTTGAGACGGAATACCTGCTTTTCA 240
DB 64072 GTCAACCGAGCGCGCTCGGTGCGCAATGCGGCTGTTGAGACGGAATACCTGCTTTTCA 64013
QY 241 CGTGAAGATGCGACGGCAATTTCCGATGAGCAAAACAAGAGAGAAAGCTGCTGTTTAAA 300
DB 64012 AAAACAAGACGGTACGGAATTTCCGCAAGCATCAGGACAGGAGGATCTGCCGCTTAAA 63953
QY 301 GAAGGTGATGCTCTGTTTATACGTTCAAAAGAAATTAACCTCAACACTTAAAGC 360
DB 63952 GAAGGTGATGCTCTGTTTATACGTTCAAAAGAAATTAACCTCAACACTTAAAGC 63893
QY 361 GAAATTCATAAACGTAATCTCTGAGGCAAGCATACCACTCGGAAATGAAAAA 420
DB 63892 AAAATCAACGAACGTAATCTCTGAGTGGGTTATCACATCGAAGAAAGAGAGAAA 63833
QY 421 TATATTTATCGTTTGTGTCAGTCCGCTTATGTTTACTA-----AAACGGAAAGAT 474
DB 63832 TATCAATATCAATTTGTCGCTGCGGCTATGTTTACCAGGCGGAGGAAAGGATAAT 63773
QY 475 GAAATTCAGAAACATCGATGAAACGAGTTTCTAATCGTTTACGCTATGACGGTTT 534
DB 63772 GAAAGAAAGAGCTCTGATGTAAGAGTTGTTTAAACGATTTAGTTATGACGGTTT 63713
QY 535 GTATATTTATTCGGAGAACATCTCTTCCAAATCTTTACGAGCGCGGAAACGGTCAATAT 594
DB 63712 GTATATTTATTCGGAGAACATCTCTTCCAAATCTTTACGAGCGCGGAAACGGTCAATAT 63653
QY 595 TCCGCAACTGGCAATATATGACCGATGCCATAGCTCATCGAGAGGTAAAGGGGTTTCC 654
DB 63652 TCCGCAACTGGCAATATATGACCGATGCCAAACGTCATCGACAGGTAAGGGGTTTCC 63593
QY 655 AGTGTGATTTGGTTATACCATATTTATGTAATGAAATTTGGGCGAGCTTCTTATGAG 714
DB 63592 AGTGTGATTTGGTTATACCATATTTATGTAATGAAATTTGGGCGAGCTTCTTATGAG 63533
QY 715 GCTAGGATCGCATGCGCGGAAAAACATCTCTGCCGAATATACGTTTAAATTTTCGAAAA 774
DB 63532 GCTAGGATCGCATGCGGAAAAACATCTCTGCCGAATATACGTTTAAATTTTCGAAAA 63473
QY 775 AAAAACCTGGAAGTAAAGTTGATTTAAATCAGTATGTGCAAAAGA-----GAGAT 825
DB 63472 AAAAACCTGGAAGTAAAGTTGATTTAAATCAGTATGTGCAAAATAAAGTAATCCAAAT 63413
QY 826 GATCTCTAAATACCATGACCATTTTCAACATTTACGCAACATTTGGACGCAACCGCTTT 885
DB 63412 GAGCCCAAAAAACCGCTGACCATTTAGCATTCGCAACATTTGGACGCAACCGCTTT 63353
QY 886 ACCGGCAGTCCCAAGAGTTAGCAGCGGAGTGAAGACGCAACACGCTGATAAGAAATTTG 945
DB 63352 ACCGGCAGTCCCAAGAGTTAGCAGCGGAGTGAAGACGCAACACGCTGATAAGAAATTTG 63293
QY 946 TTTTTCATACCGATCCGATCAGCGGCTTGGAGGCGGTTTTCGCGGATTAACGGAGAA 1005
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50	Sequence	349980 BP; 87189 A; 93501 C; 84627 G; 84663 T	0 U; 0 Other;
	Query Match	62.7%;	Score 1360.8; DB 3; Length 349980;
	Best Local Similarity	79.0%;	Pred. No. 0;
	Matches 1721;	Conservative	0; Mismatches 367; Indels 90; Gaps 5;
QY	1	ATGTGTAAACCGAATATATGGCGGCATGTCTTGTTGCCCTTACTTTTGGCATCTTGGCATC 60	
DB	99481	ATGTGTAAACCGAATATATGGCGGCATGTCTTGTTGCCCTTACTTTTGGCATCTTGGCATC 99422	
QY	61	GGCGGCAATTTTCGGGTGCGAGCTGTGTTCGTAATCAACGCCGACCGCGTACCCCGTCACT 120	
DB	99421	GGCGGCAATTTTCGGGTGCGAGCTGTGTTCGTAATCAACGCCGACCGCGTACCCCGTCACT 99362	
QY	121	TTCAAGTCTAAGGACGTGTCCACTTCGCCCCCTGCCGGGTCTTCGGTAGAAACCAACGCGG 180	
DB	99361	TTCAAAATCTAAGGACGTGTCCACTTCGCCCCCTGCCGGGTCTTCGGTAGAAACCAACGCGG 99302	
QY	181	GTCAACAGAGCCCGCTCGGTGCGGCATATCGCGCTGTTGAGACGGAATCTGCTTTTCAT 240	
DB	99301	GTCAACAGAGCCCGCTCGGTGCGGCATATCGCGCTGTTGAGACGGAATCTGCTTTTCAT 99242	
QY	241	CGTGAAGATGGCACGCAATTCGCCGATAGCAACACAGCAGAGAAAGCTGTCGTTTAA 300	
DB	99241	AAACAAGACGGTACGGAAATTTCCCGACAGCATCAGCAGAGGAGCATCTGCCGCTTAA 99182	
QY	301	GAAGGTGATGTTCTGTGTTTTATACGGTTTCAAAAGAAATAAACTTCAACAATCTAAAAAGC 360	
DB	99181	GAGNAGGATATCTGTGTTTTAGACGTACGCTGAAGACAGGCTGACAACTTAAAAAG 99122	
QY	361	GAAATTCATAAAACGTAACTCTGAGGCAAGCATTTACACATTCGGAATAAGAAATAAAAA 420	
DB	99121	AAAATCAACGNAACGGTATTTCTGATGTGAGGGTTATCACATCGAAAAAAGAAAGAAAA 99062	
QY	421	TATAATTTATCGGTTTGTCACTGCGCGTTATGTGTTTACTA-----AAACCGAAAAAGAT 474	
DB	99061	TATCAATATCAATTTGTCGTGCGGCTATGTGTTTACCAGGCGCGAAGAAAGGATAT 99002	
QY	475	GAAATTTAGAAAAACATCGGATGAAAAGCAGTTTCTTAATCGTTTAGGCTATCACGCTTTT 534	
DB	99001	GAAAAAGAAAGACTTCTGATGTGTAGGAGTTTGTTTAACGATTTAGTTATGACCGTTTT 98942	
QY	535	GTATATTTATCTCGGAGAACATCTCTCCCAATCTTTTACCAGCGCGGGAACCGTGAATAT 594	
DB	98941	GTATATTTATTCGGAGAACGTCCTTCCCAATCTTTTACCAGCGCGGGAACCGTGAATAT 98882	
QY	595	TCCGGCAATCGGCAATATATGACCGATGCCATACGTCTCGAGAGGTAAAGGGGTTTCC 654	
DB	98881	TCCGGTAACTGGCAATATATGACCGATGCCAACGTCATCGACAGTAAAGGCGGTTTTCC 98822	
QY	655	AGTGTGGATTTGGGTTTATACCAATATATGTAATGAAATTTGGGCGAGCTTCTTATGAG 714	
DB	98821	AGTACGGAATTTGGTTTATACCAATATATGTAATGAAATTTGGGCGCACTTCTTATGAG 98762	
QY	715	GCTAGGATGCCGATGGCGGGAAAAACATCTCTGCCGAATATACCGTTTAATTTCCACAAA 774	
DB	98761	GCTAGGATGCCGACGACAGGAAAAAGCATCTCTGCCGAATATACCGTTGATTGTTGATAAC 98702	
QY	775	AAAAACCTGGAAGGTAAAGTTGATTAATAATCAGTATGTCGCAAGA-----GAGAT 825	
DB	98701	AAAAACCTGGAATGGCAAGCTGATTAATAATCAGTATGTCGCAATAATAAGTAATCCAAT 98642	
QY	826	GATCTTAAAAATCCACTGACCATTTCAACATTTACCGCAACATTTGACGGCAACCGCTTT 885	
DB	98641	GAGCCCAAAAAACCGCTGACCATTTACGATTTACCGCAACATTTGACGGCAACCGCTTT 98582	
QY	886	ACCGGCACTGCCAAAGTTAGCACCGAGGTGAAGACGCAACACGCTGATAAGAAATTTTG 945	
DB	98581	ACCGGCACTGCCAAAGTTAGCACCGAGGTGAAGACGCAACACGCTGATAAGAAATTTTG 98522	
QY	946	TTTTTTCATACCGATGCCGATTCAGCGGCTTGAAGGCGGTTTTTTTTCGCGCATTAACGAGAA 1005	
DB	98521	TTTTTTCATACCGATGCCGATTCAGCGGCTTGAAGGCGGTTTTTTTTCGCGCATTAACGAGAA 98462	

2086 TTGGTGGTAATATTATTCAGACAGTACCGGAAATCGCGGTGGTATTTCGGTGGCAAGAA 2145
 97456 TTGGCGGTATATTTCATTAATGAUGGAAATCTCTTGGTATAACTGAAGAGTACTGAA 97397
 2146 GATATGACGAGGTGGAA 2163
 97396 AATAAAGTTGATGTGAA 97379

RESULT 7
 AAX23319
 ID AAX23319 standard; cDNA; 2277 BP.
 AC AAX23319;
 XX
 DT 11-JUN-1999 (first entry)
 XX
 DE N. meningitidis strain BNCV LbpB cDNA.
 KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
 KW meningitis; diagnosis; treatment; ds.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 CDS 100..2277
 /tag= a
 /product= "LbpB"
 XX
 FN MO9909176-A1.
 XX
 XX 25-FEB-1999.
 XX
 XX 10-AUG-1998; 98WO-EP005117.
 XX
 PR 15-AUG-1997; 97GB-00017423.
 PR 05-FEB-1998; 98GB-00002544.
 XX
 XX (UUT-) RIJKSUNIV UTRECHT.
 XX (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
 XX
 XX Pettersson-Fernholm AM, Tommassen JPM;
 XX
 DR WPI; 1999-190165/16.
 DR P-PSDB; AAW93492.
 XX
 PT New lactoferrin-binding protein B polynucleotides - obtained from
 PT Neisseria meningitidis, used to develop products for the diagnosis,
 PT prevention and treatment of neisserial disease, e.g. meningitis.
 XX
 PS Claim 2; Page 74-78; 116pp; English.
 XX
 CC This invention describes novel lactoferrin-binding protein B (LbpB)
 CC strains of Neisseria meningitidis. The products of this invention can be
 CC used for vaccinating humans against neisserial disease e.g. meningitis.
 CC Antibodies raised against the proteins of the invention can be used for
 CC diagnosing or treating neisserial disease in humans. The LbpB
 CC polypeptides can also be used for identifying compounds which inhibit the
 CC polypeptides
 XX
 SQ Sequence 2277 BP; 700 A; 469 C; 573 G; 535 T; 0 U; 0 Other;
 Query Match 60.2%; Score 1304.8; DB 2; Length 2277;
 Best Local Similarity 79.1%; Pred. No. 0;
 Matches 1675; Conservative 0; Mismatches 332; Indels 111; Gaps 6;
 1 ATGTGTAACGAATTATGGCGCATTTCTTGTGCGCTTACTTTTGGCATCTTGATC 60
 100 ATGTGTAACGAATTATGGCGCATTTCTTGTGCGCTTACTTTTGGCATCTTGATC 159
 61 GGCGGCAATTTCCGGTGGCGGCTGTTGCGAATCAACGCGGCGGTACCCGCTCACT 120
 160 GGCGGCAATTTCCGGTGGCGGCTGTTGCGAATCAACGCGGCGGTACCCGCTCACT 219

QY 121 TTCAAGTCTAAGACGTTCCCACTTCGCCCTCCCGGCTCTTCGGTAGAAACACACGCG 180
 Db 220 TTCAAGTCTAAGACGTTCCCACTTCGCCCTCCCGGCTCTTCGGTAGAAACACGCG 279
 QY 181 GTCAACACGCGCGCTCGGTGGCGCAATTCGGTGTGTGAGAGGAATACGCTTTTCAT 240
 Db 280 GTCAACGCGCGCGCTCGGTGGCGCAATTCGGTGTGTGAGAGGAATACGCTTTTCAT 339
 QY 241 CGTGAAGATGGCACGGCAATTCGGATAGCAAAACAGCAGAGAAAGCTCTCGTTTAAA 300
 Db 340 CGTGAAGATGGCACGGCAATTCGGATAGCAAAACAGCAGAGAAAGCTCTCGTTTCAA 399
 QY 301 GAAGTGTATGTTCTGTTTATACGGTTCAGAAAGAAATTAACCTCAACAATTTAAAGC 360
 Db 400 GAAGTGTATGTTCTGTTTATACGGTTCAGAAAGAAATTAACCTCAACAATTTAAAGC 459
 QY 361 GAAATTCATAAACGTAATCTCGAGGCAAGCAATACCAATCGGAAATGAAATTAATAAAA 420
 Db 460 GAAATTCATAAACGTAATCTCGATGTAGAAATTAGGACATCAGAAAGGAAATTAATAAAA 519
 QY 421 TATAATTATCGGTTTGTGTCAGTGGCGGTATGTGTTTACTAAAAACGGAAGAGTAAAT 480
 Db 520 TATGATTTATAAATTTGTAGATGCAGTTATGTAT---ATGTAAGGGAAGATCAAT 576
 QY 481 GAGAAACATCGGATGAAAGCAGTTTCTAATCGTTTAGCTATGCGTTTGTATAT 540
 Db 577 AAGTGGACTTCAGATTCAAGCAGTTTTCACACCGCTTAGGTATGACGGTTTGTATAT 636
 QY 541 TATCTCGAGAAACATCTTCCCAATCTTTACCGAGCGGGAACGGTGAATATTTCCGCG 600
 Db 637 TATTCGGAGAACGTCCTTCCCAATCTTTACCGAGTGGGGAACGGTGAATATTTCTG 696
 QY 601 AACTGGCAATATATGACCGATGCGATGCGATGCGAGAGTAAAGGGGTTTCCAGTGTG 660
 Db 697 AACTGGCAATATATGACCGATGCGATGCGATGCGAGAGTAAAGGGGTTTGGCATTTG 756
 QY 661 GATTTGGGTTATACCATATTTAGTAATGTAATGTAATGCGGAGCTTCTTATGAGCTAG 720
 Db 757 AATTTGGGTTATACCATATTTAGTAATGTAATGTAATGCGGAGCTTCTTATGAGCTAG 816
 QY 721 GATCCGATGGCGGAAACATCTTCCCAATCTTTACCGAGCGGGAACGGTGAATATTT 780
 Db 817 GATCTCGACGAAAGGGAACATCTTCCCAATCTTTACCGAGTGGGGAACGGTGAATAT 876
 QY 781 CTGGAAGTAAAGTTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCTTAATAATCC 840
 Db 877 CTGACGGCGAGCTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCTTAATAATCC 933
 QY 841 CTGACCAATTTACACATTTACCGCAATTTGAGCGCAACCGCTTTACCGCAGTGCCAAA 900
 Db 934 CTGACCAATTTACACATTTACCGCAATTTGAGCGCAACCGCTTTACCGCAGTGCCAAA 993
 QY 901 GTTAGCACCGAGGTGAAGACGACACGCTGATAAAGAATATTTTGTTCATACCGAT 960
 Db 994 GTCAATCTGATTTAGCGAAAGCCATGCGCAATAAGGAGCATTTGTTTTCATGCGCAT 1053
 QY 961 GCGCATCAGCGCTTGAAGCGGCTTTTTCGGGATTAACGAGAGAGCTTTCGCGCGCG 1020
 Db 1054 GCGCATCAGCGCTTGAAGCGGCTTTTTCGGGATTAACGAGAGAGCTTTCGCGCGCG 1113
 QY 1021 TTTTATCAGTAACGACACGCGTATTCGGCGTGTTCGACGCAACCAAAACAGAGACA 1080
 Db 1114 TTTTATCAGTAACGACACGCGTATTCGGCGTGTTCGACGCAACCAAAATAGCC----- 1168
 QY 1081 GCAACGATCAGATACAAATCTTCGCCCTCCCGCTGCGGAAACACACCAAAATCTTGGAT 1140
 Db 1169 -----CGTCCGCTCGGAAACACACCAAAATCTTGGAT 1203
 QY 1141 TCTCTAAATTTCCGTTGACGCGGCTGATGACCATCCCGTAAAGTTTGGCATTTCC 1200
 Db 1204 TCTCTAAATTTCCGTTGATGAGGCAAGTGGTGAATTTCCCGACCGCTTGTCCATTCT 1263

QY 1201 ACTATGCGCCGATTTGCTCATCCCGACAAACTTCTTGTGCAAGGGCGTGAATTCCTTTG 1260
 Db |||||
 QY 1264 CCTATGCGCCGATTTGCTCATCCCGACAAACTTCTTGTGCAAGGGCGTGAATTCCTTTG 1323
 Db |||||
 QY 1261 GTTAGCCAAAGAGAAACCATCGAGCTTGCAGCGGAGGAAATGACCATCGTGTGTGT 1320
 Db |||||
 QY 1324 GTTAGCCAAAGAGAAACCATCGAGCTTGCAGCGGAGGAAATGACCATCGTGTGTGT 1393
 Db |||||
 QY 1321 TGCATTTCTTGACCTATGTGAATCTCGACGGGATAAAACCGACCGCCCGCGTCAAA 1380
 Db |||||
 QY 1384 TGCACATTTTTCGACCTATGTGAATCTCGACGGGATAAAACCGACCGCCCGCGTCAAA 1443
 Db |||||
 QY 1381 CCGAAGCGGAGGATGAAGAGATTCGACATTCGATATGCGGAGGAAAGCGGAGAGAA 1440
 Db |||||
 QY 1444 CCGAAGCGGAGGATGAAGAGATTCGACATTCGATATGCGGAGGAAAGCGGAGAGAA 1503
 Db |||||
 QY 1441 ATTTCGAAGATGATAACGCGGAGATGAATGACCGAAGAGAGAGAGCTGAAGAAAC 1500
 Db |||||
 QY 1504 ATCGCGATGAAGAGAGAGACCGAGATGACCGCGGAGATGAAGAGAGAGAA 1563
 Db |||||
 QY 1501 GAAGAGAAATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1560
 Db |||||
 QY 1564 GACGAGCCACAGAAACGAGAGCGGAGAA 1596
 Db |||||
 QY 1561 ACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACT 1620
 Db |||||
 QY 1597 -----GACGAGCTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACT 1641
 Db |||||
 QY 1621 GCGGTTTACGCGAGATCTTCCGACCTCCGAGAGCTCTAAAGCGAGGACATCGACTT 1680
 Db |||||
 QY 1642 GCGATTTCAACGCGATCTTCCGAGAGCTCTAAAGCGAGGATGATCGACTT 1701
 Db |||||
 QY 1681 TTCTGAAGATTCGCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1740
 Db |||||
 QY 1702 TTCTGAAGATTCGCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1761
 Db |||||
 QY 1741 ACCGCGATTTGGAAGCGCTATCGGCTCGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
 Db |||||
 QY 1762 ACCGCGATTTGGAAGCGCTATCGGCTCGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1818
 Db |||||
 QY 1801 ACTACGTTCAATCAAAAGAGATGATGCGAATCAAGCGGAGAGAGAGAGAGAGAGAGAGAT 1860
 Db |||||
 QY 1819 -----AAAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1848
 Db |||||
 QY 1861 GATTTGTCGAGAGCTTTTTCAGTAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
 Db |||||
 QY 1849 GATTTGTCGAG 1908
 Db |||||
 QY 1921 TTTTATATCAAAAGAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
 Db |||||
 QY 1909 TTCCGATTTGAAACCGCGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1968
 Db |||||
 QY 1981 GAAATGTTGTTGATTTGTCGAG 2040
 Db |||||
 QY 1969 GATGAGGATTCGACCTTTCCGAT 2028
 Db |||||
 QY 2041 AATCTTCTGTAAGAGAGAGATTTATGTCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAT 2100
 Db |||||
 QY 2029 GATCTTCTGTAAGAGAGAGATTTATGTCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAT 2088
 Db |||||
 QY 2101 ATCGAGAGTCAACGAGAA 2118
 Db |||||
 QY 2089 TTCAATATGAGGAGAA 2106
 Db |||||

RESULT 8

AA23322

ID AA23322 standard; cdna; 2262 BP.

XX AA23322;

AC AA23322;

XX 11-JUN-1999 (first entry)

XX

DE N. meningitidis strain M990 LbpB cDNA.

XX LbpB; lactoferrin binding protein; vaccine; neisserial disease;

KW meningitis; diagnosis; treatment; ds.

XX Neisseria meningitidis.

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(CHIR) CHIRON CORP.

PA Frazier CM, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 PI Rappuoli R, Pizza M;
 XX
 DR WPI; 2000-318079/27.

XX Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
 PT in the diagnosis and treatment of *N. meningitidis* infection and other
 PT *Neisseria* infections, for example, *N. gonorrhoea*.
 XX

PS Claim 7; Page 582-586; 1760pp; English.

XX The present invention describes methods of obtaining immunogenic proteins
 CC from *Neisseria* genomic sequences. AA81453 to AA82414 represent
 CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;
 CC AA81260 to AA81303 and AA825620 to AA825663 represent *Neisseria* DNA
 CC sequences and their corresponding proteins; AA81254 to AA81259 and
 CC AA81304 to AA81321 represent PCR primers used in the isolation of
 CC *Neisseria meningitidis* DNA sequences; and AA81322 to AA81452 represent
 CC *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to *Neisseria* bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against *Meningococcus B*; against all serotypes; and/or against all
 CC pathogenic *Neisseriae*. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious *Meningococcus B*
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions
 XX

SQ Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;

Query Match	40.0%;	Score 868.2;	DB 3;	Length 14652;
Best Local Similarity	77.5%;	Pred. No. 2.3e-207;		
Matches 1141;	Conservative	0;	Mismatches 248;	Indels 84; Gaps 4;

QY	700	GCAGCTTCTATAGGCTAGGATGCCGATGCGCGGAAACATCTCCGGAATATACG	759
DB	14652	GCACTTCTTATGAGGCTAGGATGCCGACGACAGGGAAGCATCTCGCGAATATACG	14593
QY	760	GTAAATTCGACAAAAAACCTCGAAGTTAAGTTGATTAATAATCAGATGTGCAAAAG	819
DB	14592	GTTGATTTTGATAACAAAACCTGAATGGCAAGCTGATTAATAATCAGATGTGCAAAAT	14533
QY	820	A-----GAGATGATCTTAAAAATCCACTGACCATTTTACAATTTACCGCAACATTG	870
DB	14532	AAAGTAATCCAAATGAGCCCAAAAACCGCTGACCATTTACGCATTTACCGCAACATTG	14473
QY	871	GACGGCAACCGCTTTACCGCAGTGCCTAAAGTTAGCACCGAGGTGAAGACCAACAGCT	930
DB	14472	GACGGCAACCGCTTTACCGCAGTGCCTAAAGTTAGCACCGAGGTGAAGACCAACAGCT	14413
QY	931	GATAAAGAAATTTGTTTTCATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTC	990
DB	14412	GATAAAGAAATTTGTTTTCATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTC	14353
QY	991	GGCGATAACGAGAGAGCTTTCGCGCGGTTTATCAGTAACGACCAACAGCGTATTCGGC	1050
DB	14352	GGCGATAACGAGAGAGCTTTCGCGCGGTTTATCAGTAACGACCAACAGCGTATTCGGC	14293
QY	1051	GTGTTCCAGGCAACAAAAACAGACAGCAACAGCATCAGATACAAATCTTCGCCCTG	1110
DB	14292	GTATTCGAGGCAACAAAAACAGACAGCAACAGCATCAGATACAAATCTTCGCCCTG	14233

QY	1111	CCGCTCTGGAACACACACAAAATCTTGATTTCTTAAATTTCCGTTGACGAGCGACT	1170
DB	14232	TCGCTCTGGAACACACACAAAATCTTGATTTCTTAAATTTCCGTTGACGAGCGACT	14173
QY	1171	GATGACCATGCCGTAAGTTTGGCCATTTCCATATGCGCGATTTTGGTTCATCCGCAAAA	1230
DB	14172	GATAAAAATCCCGCTGAGTTTGGCCATTTCCATATGCGCGATTTTGGTTCATCCGCAAAA	14113
QY	1231	CTTCTTGTGCGAAGGCGGTGAAATTCCTTTGGTTAGCCAGGAAACCATCAGCTTCC	1290
DB	14112	CTTCTTGTGCGAAGGCGGTGAAATTCCTTTGGTTAGCCAGGAAACCATCAGCTTCC	14053
QY	1291	GACGCGAGAAAATGACCATCCGTGCTTTGTTGCGATTTTCTGACCTATGTGAAAATCGGA	1350
DB	14052	GATGCTAGAAAACGACAAATCCGAACCTGCTGCGATTTTCTGACCTATGTGAAAATCGGA	13993
QY	1351	CGGATAAAAACGACCGCCCGCTTCAACCGAAGGCGCGAGATGAAGAGGATTCGGAC	1410
DB	13992	CGGATGCAAAACGACCGCTTCCCGCGCCAAACCGAAGGCGCGAGATGAAGAGGATTCGGAC	13933
QY	1411	ATTGATATATGCGAAGAAAGCGAAGCGAAATTTCCGAAGATGATAACGCGCGAAGATGAA	1470
DB	13932	GAGGATACAGCGGTTGATAGCTCGAAGAA-----GGCGAAGACGAA	13891
QY	1471	GTACCGGAGAGAGGAGCTGAAGAAACCGAAGAAAGAACTGATGAAGACGAAGAGGAA	1530
DB	13890	ATCGACGATGAAGAGGCGACCGAAGACGACCGCTGAAAGACGAAGGCGAGGAGAGAC	13811
QY	1531	GAACCGGAGAACTGGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACT	1590
DB	13830	GAACCGGAGAACTGGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACT	13795
QY	1591	GAAGAAAATCCGCGACAGAAAGGCAACCGCGGTTTCAGGACGATCTCTCCCATCTCG	1650
DB	13794	GAAGAGAACTCCGCGACAGAAAGGCGGAGCGGTTTCAGGACGATCTCTCCCATCTCG	13735
QY	1651	GAACGCTCTAAGGCGAGGACATCGACCTTTCTCTGAAAGGTATCCGACCGCGGAAGCC	1710
DB	13734	GAACGCTCTAAGGCGAGGACATCGACCTTTCTCTGAAAGGTATCCGACCGCGGAAGCC	13675
QY	1711	GACATTCGCGAAATGGAAGACGCTATACCGGCACTTGGGAAGCGCGATCGCGGTG	1770
DB	13674	GATATTCGGAACCTGGAAGACGACACTATACCGGCACTTGGGAAGCGCGATCGCGCAA	13615
QY	1771	CCGATGAAGAAAGCGCAACGAGCTAGATGGCACTACGCTCCATTCATAAAGGATAGCTATCG	1830
DB	13614	CCCATTCATGGGACATCAGGCGGAT-----	13588
QY	1831	AATCAAGCGCAAAAGCAGAAATTTGACGTTGATTTTGGTGCAGAGTCGCTTTCAGGTAAG	1890
DB	13587	AAAGAACGCAAAAGCAGTATTTACCGTTGATTTTCGGAAGAAATCGATTTCCGGAACG	13528
QY	1891	TTGACAGAAAATGATGATACACCCCGCTTTTATTTATTTGAAAAGGTGATGATGCG	1950
DB	13527	CTGACGAGGAAAACCGGTAGAACCTGCTTCCATATTTGAAAACGCGCAAGTTTGGGC	13468
QY	1951	AACGTTTCCACGCTTGGCGCGTACTCTGTAAGAAATGCTGTTGATTTGCTGGCAAGT	2010
DB	13467	AAACGTTTCTACGCGACAGCACGCTCCGGAAGAAATCGATTTTCGGAAGTTTGGT	13408
QY	2011	TCGACTAATCCCAAGTTTAAAGCCAGTAATCTTTCTCGTAGAAGGAGGATTTTATGTT	2070
DB	13407	TCGACCGACCCCAAAACCTTCCAAAGCTAGTAAATCTTCGTAGAGGGGATTTTACGCG	13348
QY	2071	CCGACGCGCAGAGTTGGTGTGATATATATCGACAGTACCGGAAATTCGGCGTGGTA	2130
DB	13347	CCGACGCGCAGAGTTGGTGTGATATATATCGACAGTACCGGAAATTCGGCGTGGTA	13288
QY	2131	TTCCGTTCCGAAGAAAGATATGACGAGGAGGTGAA	2163
DB	13287	ACTGAAGTACTGAAATAAAGTTGATTTGATTTGAA	13255

RESULT 10
ID AAA81815 standard; DNA; 707 BP.
XX AC AAA81815;
XX DT 04-DEC-2000 (first entry)
XX DE N. meningitidis partial DNA sequence gnm_362 SEQ ID NO:362.
XX NEisseria meningitidis; Neisseria gonorrhoea; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; ds.
XX OS Neisseria meningitidis.
XX PN WO200022430-A2.
XX PD 20-APR-2000.
XX PF 08-OCT-1999; 99WO-US023573.
XX PR 09-OCT-1999; 98US-0103794P.
XX PR 30-APR-1999; 99US-0132069P.
XX PA (CHIR) CHIRON CORP.
XX Frazier CM, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
XX WPI; 2000-318079/27.
XX
PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
PT in the diagnosis and treatment of N. meningitidis infection and other
PT Neisserial infections, for example, N. gonorrhoea.
XX Claim 7; Page 1606; 1760pp; English.
XX
CC The present invention describes methods of obtaining immunogenic proteins
CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
CC specifically claimed Neisseria meningitidis genomic DNA sequences;
CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to Neisserial bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against Meningococcus B; against all serotypes; and/or against all
CC pathogenic Neisseriae. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious Meningococcus B
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions
XX
SQ Sequence 707 BP; 199 A; 155 C; 178 G; 173 T; 0 U; 2 Other;
Query Match 22.7%; Score 491.6; DB 3; Length 707;
Best Local Similarity 81.9%; Pred. No. 3.1e-113;
Matches 579; Conservative 1; Mismatches 121; Indels 6; Gaps 1;
XX 23 GCATTCGTCCTGTCCTTACTTTTGGCATCTTGGCATCGGCGCAATTCGGCGTCAGC 82

Db 1 GCATTCGTCCTGTCCTTACTTTTAGCATCTTGTATCGGCGCAATTCGGCGTCAGC 60
Qy 83 CTGTTGTGGAATCAACCGCGACCGGTACCCCGTACCTTTCAAGTCTTAAGACGTTCCCA 142
Db 61 CTGTTGTGGAATCAACCGCGACCGGTACCCCGTACCTTTCAAGTCTTAAGACGTTCCCA 120
Qy 143 CTTGCGCCCTGCGCGGTCTTCGGTAGAAACACGCGGTCAACCGCGCGCGCGTCGGTG 202
Db 121 CTCGCGCCCTGCGCGGTCTTCGGTAGAAACACGCGGTCAACCGCGCGCGCGTCGGTG 180
Qy 203 CGGCAATCGGCTGTTGAGACGGAATCTGCTTTTCAATGCGTGAAGATCGCGCAATTC 262
Db 181 CGGCAATCGGCTGCGAAGCGGAATATTGCTTCTATAAACAAGACGCTACGGAATTC 240
Qy 263 CGATAGCAACAAGACGAGAAAGCTGTGTTTAAAGAGGTGATGTTCTGTTTTAT 322
Db 241 CCGACAAGCATCAGCAGAGGAGCATCTCGCGCTTAAAGAGAGGATATCTGTTTTAG 300
Qy 323 ACGGTTCAAAAGAAATAAACTTCAACAACCTTAAAGCGAAATTCATAAACGTAATCTG 382
Db 301 ACGGTACGCTGAAGACAGAGCTGACAACTTAAAGAGAAATCAACGAGTATCTG 360
Qy 383 AGGCAAGCATTACCAATCGGAAATGAATAAATAATAATTAATTCGGTTTGTTCAGTG 442
Db 361 ATGTGAGGGTTATCACATCGAAAGAAAGAAAGAAATATCAATATCAATTTGTCGTG 420
Qy 443 CCGGTTATGCTTTACTA- ----AAAACGGAAGATGAATTCGAGAAACATCGGATG 496
Db 421 CCGGTTATGCTTTTACCAGGCGGAAAGAGATGAATGAAGAAAGAAAGATCTTCGATG 480
Qy 497 AAAAGCAGTTTCTAATCGTTTAGCTATGACGGTTTGTATATATATTCGAGAACATC 556
Db 481 GTAAGGAGTTTGTAAACGATTTAGTTATGACGGTTTGTATATATTCGAGAACATC 540
Qy 557 CTTCCCAATCTTACCGAGCGGGAACGGTGAATATTCGGGCACTTCGGCAATATATGA 616
Db 541 CTTCCCAATCTTACCGAGCGGGAACGGTGAATATTCGGTAACTTCGGCAATATATGA 600
Qy 617 CCGATGCCATAGCTCATCGGAGAGTGAAGGGGTTTCCAGTGTGGATTTGGGTTATACCA 676
Db 601 CGATGCCAAACGTCATCGGACANGTAAGGGCGGTTTCAGTACGGATTTGGGTTATACCA 660
Qy 677 CATATTATGTAATGAAATTTGGGCGAGCTTCTTATGAGGCTAGGGAT 723
Db 661 CATATTATGTAATGAAATTTGGGCGCACTTCTTATGAGGCTAGGGAT 707
RESULT 11
AAF91389
ID AAF91389 standard; DNA; 1000 BP.
XX AAF91389;
AC AAF91389;
XX 04-MAY-2001 (first entry)
XX N. meningitidis (serogroup B) LbpA gene upstream sequence, SEQ ID:15.
KW Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine;
KW genetically modified; protective antigen expression; LPS detoxification;
KW LPS; lipid A; homologous recombination vector; immunisation;
KW immunoprotective; non-toxic; paediatric; cyclic; circular; ds.
OS Neisseria meningitidis.
XX WO200109350-A2.
XX PD 08-FEB-2001.
XX PF 31-JUL-2000; 2000WO-EP007424.
XX PR 03-AUG-1999; 99GB-00018319.
XX

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Berthet FJ, Dalemans WLJ, Dencel P, Dequesne G, Feron C, Lobet Y;
Poolman J, Thiry G, Thonnard J, Voet P;

WPI; 2001-138654/14.

New isolated polynucleotide useful for outer membrane vesicle preparation
from Gram-negative bacterial strain for vaccination of microbial
infections.

Claim 46; Page 81; 128pp; English.

The invention relates to a genetically-engineered outer membrane vesicle
(bleb) preparation from a gram-negative bacterium for use as a vaccine.
The blebs of the invention are improved with respect to their
immunogenicity and toxicity by the introduction of one or more genetic
changes to the chromosome of the bacterium from which the blebs are
derived. The changes made include the upregulation of protective antigen
expression, the downregulation of immunodominant non-protective antigen
expression, and genetic changes which result in detoxification of the
Lipid A moiety of lipopolysaccharide (LPS). The invention also
encompasses modified Gram-negative bacterial strains from which the bleb
preparations are made, a vector suitable for performing recombination
events (for the generation of the modified bacterial strains),
bacterially-derived nucleic acid sequences used in such a vector, and an
immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole
cell vaccine suitable for paediatric use. The bleb preparation is useful
in the manufacture of a medicament for immunising a human host against a
disease caused by infection of one or more of the following: *Neisseria*
meningitidis, *Neisseria gonorrhoeae*, *Haemophilus influenza*, *Moraxella*
catarrhalis, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, and *Chlamydia*
pneumoniae. The invention may also be used to provide immunisation against
the influenza virus. Bacterially derived nucleotide sequences of the
invention are used in the performance of homologous recombination events
up to 1000 bp upstream of a bacterial chromosomal gene in order to either
increase or decrease expression of that gene. Immunoprotective and non-
toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more
immunogenic, less toxic and safer, and are particularly useful for
paediatric use. The present sequence represents a specifically claimed
Neisseria meningitidis nucleic acid sequence

Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;

Query Match 20.2%; Score 439.2; DB 4; Length 1000;

Best Local Similarity 71.4%; Pred. No. 5.4e-100;

Matches 681; Conservative 0; Mismatches 203; Indels 70; Gaps 5;

1210 GATTTTGGTTCATCCCGACAAACTTCTTGTGGAAGGGGTGAAATTCCTTTGGTTAGCCAA 1269
1 GATTTTGGTTCATCCCGACAACTTCTTGTGGAAGGGGTGAAATTCCTTTGGTTAGCCAA 60

1270 GAGAAACCCATCGAGTTGCGAGCGGAGGAAATGACCATCCGTGCTTGTGCGATTTT 1329
61 GAGAAACCCATCGAGTTGCGAGCGGAGGAAATGACCATCCGTGCTTGTGCGATTTT 120

1330 CTGACCTATGTAACCTCGAGCGGATAAACCCAGCCGCCCGCTCAACCGAAGCG 1389
121 TTGACCTATGTAACCTCGAGCGGATAAACCCAGCCGCCCGCTCAACCGAAGCG 180

1390 CAGGATGAAGAGGATTCGGACATTGATAATGGCGAAGAAAGCGAAGCAATTCGGAA 1449
181 GAAGATAAAGGGA-----GGATGAAGAGATGCGAGG 213

1450 GATGATAACCGCGAAGATGAAGTCAACCGAAGAGGAAGCTGAAGAAACCGAAGAGAA 1509
214 GTTGGTAACCTCGAAGAG-----GCGAAGGCGAAGTTCCGNAGATGAAGCGAAGAA 267

1510 ACTGATGAACGACGAGGAGAGAACCCGAGAAACTGAAGAACTGAAGAACTGAAGAA 1569
268 GCCGAAGAAATCGTCGAAGAGAGAACCCGAGAACTGAAGAGGAAGAGCT---GAA 324

1570 ACTGAAGAAACTGAAGAACTGAAGAAATTCGCCGACAGAGNAGCGCAACGGCGGTCA 1629

Db 325 CCCAAGAAGTTGAAGAAACCGAAGAAATCCGCCACAGAAGAAAGCGGCGTTCA 384
QY 1630 GCGAGCATCTCCGCCACTCCGGAAGCTCTAAAGGCGAGGACATCGACCTTTTCTTGAAA 1689
Db 385 AACGCATCTCTCCCTCGGAGCCTCTAAAGGCGAGGACATCGACCTTTTCTTGAAA 444
QY 1690 GGTATCCGACGCGGGAAGCGGACATTCGCAAAATTGGAAGAGCGCTATATACCGGCACT 1749
Db 445 GGTATCCGACGCGGGAAGCGGACATTCGCAAAATTGGAAGAGCGCTATATACCGGCACT 504
QY 1750 TGGGAAGCGGCTATCGGCGTCCGAGTAAGAAAGCGGACAGCTAGATGGCACTACGTCC 1809
Db 505 TGGGAAGCGGCTATCGGCGTCCGAGTAAGAAAGCGGACAGCTAGATGGCACTACGTCC 552
QY 1810 ATTCAAAAGGATAGCTATCGGCGTCCGAGTAAGAAAGCGGACAGCTAGATGGCACTACGTCC 1869
Db 553 -----AAGAGCGGCGAAGAGCAAGATTTACCGTTAAATTTCCG 591
QY 1870 GCGAAGTCGTTTTCAGGTAAGTTGACAGAAATAATGATACACACCCCGCTTTTATATT 1929
Db 592 GAGAAATCGATTTCCGGAACGCTGAGCGGAGAAACCGGTGTACAACTGCTTTCTATATT 651
QY 1930 GAAAAGGTGATGATGAGCAAGCTTTCACGCTTTGGCGCGTACTCGTGAAAATCGT 1989
Db 652 GAAAACGCAAGATTTGAGGGCGACGGTTTCCACGCAACAGCAGCACTCGTGAGAACGCG 711
QY 1990 GTTGATTTGTCGGGCAAGGTTCCGACTAATCCCAAGTTTAAAGCCAGTAATCTTCTC 2049
Db 712 ATCAATCTTCGGGAATGGTTCCGACCAACCCCAAGCTTCCCAAGCTAGTGTCTCGT 771
QY 2050 GTAGAAGGAGGATTTTATGTTCCGCGAGCGGCGAGAGTTGGGTGTTAATATTATCGACAGT 2109
Db 772 GTAGAAGGAGGATTTTACGGCCCGCA-GCGAGGATTTGGCGGTATTATTTCATTAAG 830
QY 2110 GACCGGAAATTCGGCGTGGTATTTCGGTCCGGAAGAAAGATATCGAGGAGGTGAA 2163
Db 831 GATCGGAAATCTCTTGGTATAACTGAAGGTACTGAAATAAAGTTGAAGTTGAA 884

RESULT 12

ABK37769
ID ABK37769 standard; DNA; 1000 BP.

XX ABK37769;

XX AC

XX 08-MAY-2002 (first entry)

XX DE DNA sequence upstream of LbpA #1 gene.

XX DE

XX KW Upstream sequence; ds; Antibacterial; vaccine; bleb;
KW Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;
KW meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;
KW sinusitis.

OS *Neisseria meningitidis* serogroup B.

XX

XX

XX WO200209746-A2.

XX 07-FEB-2002.

XX 31-JUL-2001; 2001WO-EP008857.

XX 31-JUL-2000; 2000WO-EP007424.

XX 08-FEB-2001; 2001GB-00003170.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Berthet FJ, Dalemans W, Denoel P, Dequesne G, Feron C, Garcon N;

XX Lobet Y, Poolman J, Thiry G, Thonnard J, Voet P;

XX WPI; 2002-188688/24.

XX

CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 400 BP; 215 A; 34 C; 131 G; 19 T; 0 U; 1 Other;

Query Match 4.4%; Score 94.6; DB 5; Length 400;
 Best Local Similarity 64.0%; Pred. No. 1.6e-13;
 Matches 142; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
 QY 1378 AAACCGAAGCGCAGGATGAAGAGGATTCGGACATTGATATGCGAAGAAACCGAGAC 1437
 Db 97 AAAGGAA 156
 QY 1438 GAAATTTCCGAGATGATTAACCGCGAAGATGAAGTCACCGAAGAGAGAGAGAGAGAA 1497
 Db 157 GAAGAA 216
 QY 1498 ACCGAGAGAGAACTGATGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1557
 Db 217 GAGGAA 276
 QY 1558 GAAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAA 1599
 Db 277 GAAGAA 318

RESULT 14

AAS68580
 ID AAS68580 standard; cDNA; 963 BP.

XX AAS68580;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #4384.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-FSDB; ABG04393.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 1; SEQ ID NO 4384; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 963 BP; 353 A; 171 C; 268 G; 169 T; 0 U; 2 Other;

Query Match 4.4%; Score 94.6; DB 5; Length 963;

Best Local Similarity 64.0%; Pred. No. 2.3e-13;

Matches 142; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1378 AAACCGAAGCGCAGGATGAAGAGGATTCGGACATTGATATGCGAAGAAACCGAGAC 1437
 Db 97 AAAGGAA 156
 QY 1438 GAAATTTCCGAGATGATTAACCGCGAAGATGAAGTCACCGAAGAGAGAGAGAGAA 1497
 Db 157 GAAGAA 216
 QY 1498 ACCGAGAGAGAACTGATGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1557
 Db 217 GAGGAA 276
 QY 1558 GAAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAA 1599
 Db 277 GAAGAA 318

RESULT 15

AAS92079/c

ID AAS92079 standard; cDNA; 453 BP.

XX AAS92079;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #27883.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 12:38:10 ; Search time 157.593 Seconds
(without alignments)
7637.968 Million cell updates/sec

Title: US-10-735-098-3
Perfect score: 2169
Sequence: 1 atgtgtaaacgaattatgg.....tcagaggagtggaataatga 2169

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/ina/6A-COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B-COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS-COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	85.6	3.9	7218	1	US-08-232-463-14
C 2	85.4	3.9	929	4	US-09-671-317-14
C 3	83.4	3.8	1001	4	US-09-671-317-439
C 4	77	3.6	2223	1	US-08-257-073-4
5	73.4	3.4	43795	3	US-08-742-185-101
6	72.6	3.3	966	2	US-08-766-738-2
7	72.6	3.3	966	4	US-09-262-610-2
8	71.6	3.3	3211	2	US-08-574-959A-8
9	71.6	3.3	3211	3	US-09-357-014-8
10	71.6	3.3	3901	2	US-08-574-959A-6
11	71.6	3.3	3901	3	US-09-357-014-6
12	71.4	3.3	3489	2	US-08-728-323A-1
13	71.4	3.3	3489	4	US-09-298-568-1
14	71.4	3.3	3489	4	US-09-410-399-1
C 15	71.4	3.3	32207	2	US-08-770-379-20
C 16	71.4	3.3	32207	4	US-08-757-669A-20
C 17	71.4	3.3	32207	4	US-09-230-371A-20
18	68.6	3.2	1276	3	US-09-177-325-2
19	68.6	3.2	1276	3	US-09-411-812A-2
20	68.6	3.2	1276	4	US-09-590-113-2
21	65	3.0	696	3	US-09-461-697-193
22	65	3.0	699	3	US-09-461-697-191
23	65	3.0	717	3	US-09-461-697-189
24	65	3.0	774	3	US-09-461-697-187
25	65	3.0	819	3	US-09-461-697-185
26	65	3.0	1669	3	US-09-461-697-184
27	63.6	2.9	1236	2	US-08-741-134-5

28	63.2	2.9	390	3	US-09-197-649-7	Sequence 7, Appli
29	63.2	2.9	3955	4	US-09-976-594-207	Sequence 207, App
30	62.6	2.9	2518	3	US-09-433-699-3	Sequence 3, Appli
31	62.6	2.9	6002	4	US-09-345-882-4	Sequence 4, Appli
C 32	62.6	2.9	16442	3	US-08-781-891-208	Sequence 208, App
C 33	62.6	2.9	16442	4	US-09-618-166-208	Sequence 208, App
34	62.4	2.9	2712	4	US-09-489-039A-6521	Sequence 6521, Ap
35	62	2.9	1052	1	US-08-466-603-1	Sequence 1, Appli
36	62	2.9	1052	1	US-08-314-503A-1	Sequence 1, Appli
37	62	2.9	1052	1	US-08-468-066-1	Sequence 1, Appli
38	62	2.9	1052	2	US-08-466-717-1	Sequence 1, Appli
39	62	2.9	1052	3	US-08-466-743-1	Sequence 1, Appli
40	62	2.9	1052	5	PCT-US95-12414-1	Sequence 1, Appli
41	61.4	2.8	4226	4	US-09-620-312D-480	Sequence 480, App
42	61.2	2.8	2139	4	US-09-059-584-50	Sequence 50, Appli
43	61.2	2.8	3337	1	US-08-072-610-1	Sequence 1, Appli
44	61.2	2.8	3337	2	US-08-719-822B-1	Sequence 1, Appli
45	61.2	2.8	3337	3	US-09-092-458-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 435
; FILING DATE:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 3.9%; Score 85.6; DB 1; Length 7218;

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; Best Local Similarity 4.9%; Pred. No. 3.1e-13;
; Matches 19; Conservative 239; Mismatches 128; Indels 0; Gaps 0;
;
; 1268 AAGAGAAACCATCGAGCTTCCGACGCGAGGAAATGACCATCGCTGTTGCGGATT 1327
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1416 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1357
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1328 TTCTGACATGTAAGTAACTCGGACGATAAAACCGACGCGCCCGCTCAACCGAAG 1387
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1356 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1297
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1398 CCAGATGAAGAGATTCGACATGATAATGCGGAGAAAGCGAAGCAAGAAATTCG 1447
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1296 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1237
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1448 AAGATGATAACCGGCAAGATGAAGTCAACGAGAGAGAAAGCTGAAGAAACCGAAG 1507
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1236 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1177
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1508 AAAGTGAAGAGAGAGAGAGAACCGGAGAAAGCTGAAGAAAGCTGAAGAAAGTGA 1567
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1176 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1117
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1568 AAAGTGAAGAAAGCTGAAGAAAGCTGAAGAAAGCTGAAGAAAGCTGAAGAAAG 1627
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1116 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1057
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1628 CAGGAGCATCTCGCCCACTCGGAA 1653
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 1056 CCTCGACCTGACGCAAGCTCGAA 1031
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
;
; RESULT 2
; US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-363 : polymorphic base A or G
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-363.mis1, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-454-363.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 139..158
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind

```

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; LOCATION: 634..652
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-454-363 potential probe
; NAME/KEY: misc feature
; LOCATION: 674..679,881..882,892..893
; OTHER INFORMATION: n=a, g, c or t
; US-09-671-317-14
;
; Query Match 3.9%; Score 85.4; DB 4; Length 929;
; Best Local Similarity 60.3%; Pred. No. 1.1e-13;
; Matches 149; Conservative 0; Mismatches 96; Indels 2; Gaps 1;
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; QY 1372 GCCGTCAACCGGAGGCGCAGGATCAAGAGGATTCGGACATTGATAATGCGGAAAGAACG 1431
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; DB 909 GCACCTCCAGCCTGAGCNCAGCGANNCCATCTCAAGAGAGAGAGAGAGAGAGAA 850
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; QY 1432 GAAGACGAAATTTCCGAAAGATGATAACCGCGAAGATGAAGTCAACGAGAGAGAGAGAG 1491
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; DB 849 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; QY 1492 GAAGAAACCGAAGAGAGAACTGTATGAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; DB 789 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; QY 1552 ACTGAAGAACTGAAGAAAGCTGAAGAAAGCTGAAGAAAGCTGAAGAAAGCTGAAGAAAG 1611
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; DB 731 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; QY 1612 GAAGGCA 1618
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; DB 671 GAAGAGAA 665
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
;
; RESULT 3
; US-09-671-317-439/c
; Sequence 439, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 439
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-242 : deletion AT
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-242.mis1, potential
; NAME/KEY: primer_bind
; LOCATION: 260..279
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match
Best Local Similarity 3.4%; Score 73.4; DB 3; Length 43795;
Mismatches 128; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1378 AAACCGAGGCCGAGGATGAGGATTCGGACATTGATATGCGGAGAAAGCGAAGC 1437
DB 38833 AAAAAAAG 38892
QY 1438 GAAATTCGAGATGATAACCGCGAAGATGAAGTCAACCGAAGAGAGAGAGAGAG 1497
DB 38893 GGAGATGAG 38952
QY 1498 ACCGAGAGAGAACTGATGAGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
DB 38953 AAGGAAGCGGAG 39012
QY 1558 GAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAA 1596
DB 39013 GAAGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39051

RESULT 6
US-08-766-738-2
Sequence 2, Application US/08766738
Patent No. 5916749
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,738
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0177 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 1813361
US-08-766-738-2

Query Match 3.3%; Score 72.6; DB 2; Length 966;

Best Local Similarity 58.9%; Pred. No. 4.1e-10;
Matches 123; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1387 GCGCAGGATGAGAGAGATTCGGACATTGATATGCGGAGAAAGCGAAGC 1446
DB 571 GAGGTGGATGGTGTGTTGATNAAGANGAGGAGGAGGAGGAGGAGGAGGAG 630
QY 1447 GAAAGATGATAACGGCGAAGATCAAGTCCACCGAAGAGAGAGAGAGAGAG 1506
DB 631 GACGATGAGGATGGTGAAGAGAGAGGTTTGTATGAAGAGAGATGATGAAGATGA 690
QY 1507 GAAATCTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1566
DB 691 GAAGGGGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
QY 1567 GAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACT 1595
DB 751 GAAAGATGAGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 779

RESULT 7
US-09-262-610-2
Sequence 2, Application US/09262610
Patent No. 6428949
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,610
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,738
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0177 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 1813361
US-09-262-610-2

Query Match 3.3%; Score 72.6; DB 4; Length 966;
Best Local Similarity 58.9%; Pred. No. 4.1e-10;
Matches 123; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1387 GCGCAGGATGAGAGAGATTCGGACATTGATATGCGGAGAAAGCGAAGC 1446

Db 571 GAGGTGGATGTTGTTGATNAGANCAGGACCGAGAGGAGAGGATGAGAGACGAG 630
QY 1447 GAAGATGATACGGCGAAGATGAAGTACCGAAGAGAGGAGCTGGAAGAAACCGAAGAA 1506
Db 631 GACGATGAGGATGGTGAAGAGAGAGGAGTTTGTATGAAGAGAGATGATGAAGATGA 690
QY 1507 GAAACTGATGAG 1566
Db 691 GAAGGGATGAGGACGAGGATGAAGTCACTGAGGAGGAGAGAGAGATTTGGACTTGA 750
QY 1567 GAAACTGAAGAACTGAAGAACTGAAGA 1595
Db 751 GAAGATGAAGATGAGATGAGATGAAGA 779

RESULT 8
US-08-574-959A-8
; Sequence 8, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19-DEC-95
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
US-08-574-959A-8

Query Match 3.3%; Score 71.6; DB 2; Length 3211;
Best Local Similarity 59.2%; Pred. No. 1.5e-09;
Matches 122; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1410 CATTGATTAATGCGAAGAAACGAGACGAAATTTCCGAGATGATACGCGGAGATGA 1469
Db 2391 CAGTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2450
QY 1470 AGTCAACCGAAGAGAGGAGTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGA 1529
Db 2451 GGAAG 2510
QY 1530 AGAACCCGAGAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACT 1589
Db 2451 GGAAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2510
QY 1530 AGAACCCGAGAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACT 1589

Db 2511 TGAAGAGAGATATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTGAAGAGATTTGA 2570
QY 1590 TGAAGAGAGAAATCGCCGACAGAGAGAG 1615
Db 2571 GGAAGAGAGAGGTGAGTTAGAGAGAG 2596
RESULT 9
US-09-357-014-8
; Sequence 8, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/357,014
; FILING DATE: 19-Jul-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/574,959
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-357-014-8

Query Match 3.3%; Score 71.6; DB 3; Length 3211;
Best Local Similarity 59.2%; Pred. No. 1.5e-09;
Matches 122; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1410 CATTGATTAATGCGAAGAAACGAGACGAAATTTCCGAGATGATACGCGGAGATGA 1469
Db 2391 CAGTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2450
QY 1470 AGTCAACCGAAGAGAGGAGTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGA 1529
Db 2451 GGAAG 2510
QY 1530 AGAACCCGAGAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACT 1589
Db 2511 TGAAGAGAGATATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTTGAAGAGATTTGA 2570
QY 1590 TGAAGAGAGAAATCGCCGACAGAGAGAG 1615

APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1...3489
US-08-728-323A-1

Query Match 3.3%; Score 71.4; DB 2; Length 3489;
Best Local Similarity 56.0%; Pred. No. 1.8e-09;
Matches 135; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
QY 1385 AGGCGGAGGATGAAGAGGATTCGGACATTTGATATGCGGAGAAAGCGAAGCAAAATTT 1444
Db 1046 ACAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATG 1105
QY 1445 CCGAAGATGATGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1504
Db 1106 ACAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGAGG 1165
QY 1505 AAGAACTGTAGTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1564
Db 1166 ACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1225
QY 1565 AAGAACTGTAGTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1624
Db 1226 AGGCAATGAGGACGAGGAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1285
QY 1625 G 1625
Db 1286 G 1286

RESULT 13
US-09-298-568-1
Sequence 1, Application US/09298568
Patent No. 632792
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.

TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

Query Match 3.3%; Score 71.4; DB 4; Length 3489;
Best Local Similarity 56.0%; Pred. No. 1.8e-09;
Matches 135; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
QY 1385 AGGCGGAGGATGAAGAGGATTCGGACATTTGATATGCGGAGAAAGCGAAGCAAAATTT 1444
Db 1046 ACAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATG 1105
QY 1445 CCGAAGATGATGAAGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGG 1504
Db 1106 ACAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGAGG 1165
QY 1505 AAGAACTGTAGTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1564
Db 1166 ACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1225
QY 1565 AAGAACTGTAGTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1624
Db 1226 AGGCAATGAGGACGAGGAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1285
QY 1625 G 1625
Db 1286 G 1286

RESULT 14
US-09-410-399-1
Sequence 1, Application US/09410399
Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

Query Match 3.3%; Score 71.4; DB 4; Length 3489;
Best Local Similarity 56.0%; Pred. No. 1.8e-09;
Matches 135; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
QY 1385 AGGCGGAGGATGAAGAGGATTCGGACATTTGATATGCGGAGAAAGCGAAGCAAAATTT 1444
Db 1046 ACAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATG 1105
QY 1445 CCGAAGATGATGAAGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGG 1504
Db 1106 ACAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGAGG 1165
QY 1505 AAGAACTGTAGTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1564

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 11:49:00 ; Search time 4949.35 Seconds
(without alignments)
13086.780 Million cell updates/sec

Title: US-10-735-098-3

Perfect score: 2169

Sequence: 1 atgtgtaaacgaattatgg.....tcgaggagggtgaaaataatga 2169

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estcin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	103.6	4.8	879	28	AZ550718
C 2	103.6	4.8	881	28	AZ688514
C 3	103.6	4.8	942	28	BH148582
C 4	102.6	4.7	434	14	CA745444

5	100.4	4.6	675	28	BZ104011
6	100.2	4.6	665	13	BU432980
7	99.8	4.6	264	13	BQ241566
8	99.8	4.6	686	29	CE063557
9	99	4.6	612	28	BZ149404
10	98.8	4.6	575	10	BF707975
C 11	98.6	4.5	232	29	CG321416
C 12	98.6	4.5	880	28	AZ529191
C 13	98.4	4.5	265	14	CA607797
C 14	97.8	4.5	263	13	BG005139
15	97.6	4.5	689	28	AZ971991
16	97.6	4.5	960	28	CC143364
17	97.2	4.5	622	13	BU418103
C 18	97	4.5	233	12	BJ454017
19	97	4.5	332	14	CA566759
C 20	96.6	4.5	311	14	CA699402
21	96.6	4.5	340	13	BQ462203
C 22	96.6	4.5	739	28	BZ220379
23	96.2	4.4	871	29	CG354013
24	95.6	4.4	395	29	CE760553
25	95.6	4.4	558	12	BM163267
C 26	95.4	4.4	289	14	CA716220
27	95.4	4.4	617	14	CA743799
28	95.2	4.4	453	12	BM167376
29	95.2	4.4	459	12	BM171330
30	95.2	4.4	648	12	BM164042
31	95.2	4.4	739	12	BM160442
32	95.2	4.4	753	12	BM167115
33	95.2	4.4	790	12	BM166415
34	95.2	4.4	900	28	AZ549980
35	95.2	4.4	925	28	AZ538036
36	95.2	4.4	1030	14	CF470007
37	95	4.4	531	14	CD915362
C 38	95	4.4	546	28	AZ600777
39	94.8	4.4	799	28	BZ201507
40	94.6	4.4	596	29	CC660549
C 41	94.6	4.4	691	28	BH040136
42	94.6	4.4	953	13	BQ939407
43	94.4	4.4	617	14	CD925518
C 44	94	4.3	1096	14	CK206118
C 45	93.8	4.3	421	28	AZ113646

ALIGNMENTS

RESULT 1
AZ550718/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ550718 879 bp DNA linear GSS 14-NOV-2000
ENTEM36TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, genomic survey sequence.

AZ550718.1 GI:11176019

GSS

Entamoeba histolytica

Entamoeba histolytica

Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 879)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HMI:IMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjloftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared

DNA library

Seq primer: M13-Forward

Class: shotgun

FEATURES	Location/Qualifiers
source	1. .879

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10

/organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HMI:1MS8"
 /db_xref="taxon:5759"
 /clone_label="Entamoeba histolytica clone HMI:1MS8"
 /notes="Vector: pBOS1; Site 1: Bst
 Institute for Genomic Research (TIGR)
 Genomic DNA isolated from broth
 using a method described by Claret
 C.G., and Diamond, L.S. (1993). E.
 method for isolate identification
 tight size distribution (~2 kb).
 the library construction is described
 H.O. and Venter, J.C. (Making sm
 whole genome shotgun sequencing
 Sequencing: A Practical Approach,
 Burrell. Oxford University Press.

ORIGIN

Query Match 4.8%; Score 103.6; DB 28; Length 881;

Best Local Similarity 64.7%, Freq: NO: 0.50 11,
Matches 154: Conservative 0: Mismatches 84: Indels 0: Gaps 0:

Qy	1393	GATGAAGAGGATTCGCACATTGTAATATGGCGAAGAAGACGGAAGACAGAAATTTCCGAGAT	1452
Db	300	GACCAAGAGAAGAGATGATGAGAAGATGAGAAGATGAAGAAGATGAAGAAGATGAAGAA	241
Qy	1453	GATTAACGGCGAAGATGAAGTCCCGAAGAGAAGCGAAGCTGAAGAAACCGAAGAAAGAAACT	1512
Db	240	GATGAAGAAGATGAAGAGATGAAGAAGATGAAGAGATGAAGAAGATGAAGAAGATGAA	181
Qy	1513	GATGAAGACGAAGAGGAAGAACCCGAGAAACTCTGAAGAAACTGAAGAAACTGAAGAAACT	1572
Db	180	GAAGATGAAGAAGATGAAGAAGACGAGAAGATGAAGAAGATGAAGAAGATGAAGAAGAT	121
Qy	1573	GAGAAACTGAAGAACTGAAGAAAATCCCGACACAGAGAAGACGACCGCGTTTCAG	1630
Db	120	GAGAAGAGATGAAGAAGATGAAGAAGATGAAGAAGACGAGAAGACGAGAAGATGAAG	63

RESULT 3
BH148582

BH148582 942 bp DNA linear GSS 27-AUG-2001
ENPR62TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, genomic survey sequence.

BH148582.1 GI:15308029
GSS.

Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 942)
Loftus, B., Wang, Z., Van Aken, S. and

Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)

Unpublished (2001)
Contact: Brendan J Loftus

Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208

Fax: 301 838 3543
Email: bjloftus@tigr.org

Clones are derived from the *Entamoeba histolytica* HM1:IMSS sheared DNA library

Seq primer: M13-Forward
Class: shotgun

High quality sequence start: 15
High quality sequence stop: 794


```

/lab_host="E. coli DH10B"
/clone_lib="Tae05"
/note="vector: pSPORT-p (Invitrogen Technologies); Site.1:
NotI; Site.2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"

ORIGIN
      4.6%;   Score 99.8;   DB 13;   Length 264;
Best Local Similarity 66.5%;   Pred. No. 3.6e-10;
Matches 143;   Conservative 0;   Mismatches 72;   Indels 0;   Gaps 0;

QY 1391 AGGATGAAGAGGATTCCGACATTGCATATGCGAAGAAAGCGAAGACGAAATTTCCGAAG 1450
Db 49  AAGAAGAAGAGAGAGGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 108

QY 1451 ATGATACGGCGAAGATGAAGTACCGAAGAGAGAGAGCTGAAGAAACCCGAAGAAGAAA 1510
Db 109  AAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 168

QY 1511 CTGATGAGACGAAGAGAGAGAACCCGAGAGAACTGAAGAAACTGAAGAACTGAAGAAA 1570
Db 169  AAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 228

QY 1571 CTGAAGAAAACCTGAGGAAGTCAAGAAAAATCGCGG 1605
Db 229  AAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263

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RESULT 8	CE063557	686 bp	DNA	linear	GSS 24-SEP-2003
LOCUS	CE063557				
DEFINITION	tigr-gss-dog-17000322636088 Dog Library Canis familiaris genomic, genomic survey sequence.				
ACCESSION	CE063557				
VERSION	CE063557	GI:35117950			
KEYWORDS	GSS.				
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
AUTHORS	Kirkness, E.F., Batna, V., Halpern, A.L., Levy S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.				
TITLE	The dog genome: survey sequencing and comparative analysis				
JOURNAL	Science 301 (5641), 1898-1903 (2003)				
MEDLINE	22875432				
PUBMED	14512627				

CONTACT: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

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FEATURES
  source
    Location/Qualifiers
      1..6886
        /organism="Canis familiaris"
        /mol_type="Genomic DNA"
        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /note="Site 1: BstXI; Libraries were prepared from
        peripheral blood"

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ORIGIN

peripheral blood"

Query Match 4.6%; Score 99.8; DB 29; Length 686;
Best Local Similarity 65.6%; Pred. No. 3.9e-10;
Matches 162; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

1372 GCCGTCAACCGAAGCGCAGGATGAAGAGGATTCGACATTGATATGCCAAGAAGC 1431

Db	168	GCCTGGGCACTGTAGGGCCAGGGCGAAGGGGTCTCAGAGAAGAAGAAGAAGAA	227
Qy	1432	GAAGACGAAATTTTCCGAAGATGATAACCGCGAAGATGAAGTCAACCGAAGAGGAGGCT	1491
Db	228	GAAGAAGAAACAGAGAGAGAAACAGAGAGAGAGAGAGAACAGAGAAGAAGAAGAA	287
Qy	1492	GAAGAAACCGAAGAGAAACTGA---TGAAGACGAAGAGGAGAACCAGGAAGAACTGAA	1548
Db	288	GAAGAAGAAGAAGAAGAAGAAACTTGAAGAAGAAACAGAGAAGAAGAAGAAGAA	347
Qy	1549	GAAACTGAAGAAACTGGAAGAACTGAAGAACTTGAAGAACTGAAGAAATCCCGACA	1608
Db	348	GAAGAAGAGAGAGAGAGAACTGAAGAGAAGAAGAACTGAAGAAGAAGAAACAGAA	407
Qy	1609	GAAGAAG	1615
Db	408	GAAGAAG	414

RESULT	9
BZ149404	
LOCUS	
DEFINITION	BZ149404 CH230-395ML.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
ACCESSION	BZ149404
VERSION	BZ149404.1 GI:23790354
KEYWORDS	GSS.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
TITLE
JOURNAL
Rat BAC End Sequences from Library CHORI-230 MboI segment
COMMENT
Unpublished (1999)
Other_GSSs: CH230-395M1.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pdejongemail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html. Plate: 395 row: M column: 1
Seq primer: SP6
Class: BAC ends.

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Class: BAC ends.
Location/Qualifiers
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    /db_xref="taxon:10116"
    /clone="CH230-395M1"
    /sex="Female"
    /cell_type="Brain"
    /clone_lib="CHORI-230 Segment 2"
    /note="vector: pPARBAC1.3; Site 1: MboI;
    CHORI-230 Rat (EN/SNHsd/MCW) BAC library produced by
    Pieter de Jong"

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Query Match      4.6%; Score 99; DB 28; Length 612;
Best Local Similarity 63.0%; Pred. No. 5.6e-10;
Matches 153; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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[illegible]

RESULT 10	
BF707975	
LOCUS	575 bp mRNA linear EST 12-JUN-2002
DEFINITION	A634 LE Aplysia metacerebral cell cDNA library Aplysia californica
	CDNA '5', mRNA sequence.
ACCESSION	BF707975
VERSION	BF707975.1 GI:18002301
KEYWORDS	EST.
SOURCE	Aplysia californica (California sea hare)
ORGANISM	Aplysia californica
	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
	Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia;
	Anaspidae; Aplysioidea; Aplysidae; Aplysia.
REFERENCE	1 (bases 1 to 575)
AUTHORS	Sadreyev,R.I., Meleshkevich,E.A., Matz,M.V., Panchin,Y.V. and Moroz,L.L.
TITLE	Characterization of the gene pool expressed in the individual identified neuron
JOURNAL	Unpublished (2001)
COMMENT	Contact: Sadreyev R.I. The Whitney Laboratory University of Florida 9505 Ocean Shore Blvd., St Augustine, FL 32080, USA Tel: 904 461 4044 Fax: 904 461 4008 Email: sadreyev@whitney.ufl.edu Seq primer: 5' CCAGCTGGACTATCCATGAACGCA 3'.

[illegible][illegible]

TIGR
9712 Medical Center Drive. Rockville, MD 20850, USA

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends

FEATURES	source
Class: Source	Location/Qualifiers
	1..232
	/organism="zebra mays"
	/mol_type="genomic l
	/strain="B73"
	/db_xref="taxon:457
	/clone="ZMMBMA0640J
	/clone_lib="ZM 0.7
	/note="Vector: pBGS
	methylation filter

ORIGIN

	Query Match	4.5%;	Score 98.6;	DB 29;	Length 232;
	Best Local Similarity	64.9%;	Pred. No. 6.3e-10;		
	Matches 146;	Conservative 0;	Mismatches 79;	Indels 0;	Gaps 0;
Qy	1391	AGGATGAAGAGGATTCCGACATTGATTAATCGCGAAGAAGACGAAGACGAAATTTCCGAAG	1450		
Db	232	AGAAGAAGAAGAAGAAGACAGATGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	173		
Qy	1451	ATGATACCGCGAAGATGAACTCAGGAAGAAGAGGAAGCTGAAGAAACCGAAGAGAAA	1510		
Db	172	AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	113		
Qy	1511	CTGATGAAGACGAGAGCGGAAGACCCGAGAAACTGAAGAAACTGAAGAAACTGAAGAAA	1570		
Db	112	AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	53		
Qy	1571	CTGAAGAAAACCTGAAGAAACTGAAGAAAATCGCCGACAGAGAAG	1615		
Db	52	AAGAGAGAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	8		

[illegible]

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genomic, genomic survey sequence.
ACCESSION AZ529191
VERSION AZ529191.1 GI:11081835
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
REFERENCE Entamoeba histolytica
AUTHORS Eukaryota; Entamoebidae; Entamoeba.
TITLE 1 (bases 1 to 880)
JOURNAL Loftus B., Van Aken, S. and Fraser, C.
COMMENT Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 673.
FEATURES
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        Institute for Genomic Research (TIGR), Rockville, MD.
        Genomic DNA isolated from broth cultures of E. histolytica
        using a method described by Clark and Diamond (Clark,
        C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
        method for isolate identification. Exp. Parasitol.
        77:450.). The DNA was mechanically sheared to give a
        tight size distribution (~2 kb). The v + i method used for
        the library construction is described in detail in Smith,
        H.O. and Venter, J.C. (Making small insert libraries for
        whole genome shotgun sequencing projects. In Genome
        Sequencing: A Practical Approach, eds. M. Vaudin and B.
        Barel, Oxford University Press, 1999)."
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Query Match 4.5%; Score 98.6; DB 28; Length 880;
Best Local Similarity 64.9%; Pred. No. 7e-10;
Matches 146; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1391 AGGATGAGAGGATTCGACATTGATATCGCGAAGAGGAGCGAGACGAAATTCGGAAG 1450
Db 698 AAGACGAGCGAGCGAAGATGACGAGAGGAGCGAGACGAGAGGAGAGGAGAGGAGAG 639

Qy 1451 ATGATACCGCGAGAGTGAAGTCCGAGAGAGGAGCTGAAGAACCGAGAGAGAA 1510
Db 638 AAGAGAGAGCGAGAGAGAGAGAGAGCGAGAGAGATGAGACGAGAGATGAAGACGAG 579

Qy 1511 CTGATGAGAGCGAGAGAGAGAACCCGAGAGAACTGAAGAACTGAAGAAA 1570
Db 578 AAGATGAGAGCGAGAGAGATGAAGACGAGAGAGATGAAGACGAGAGATGAAGACGAG 519

Qy 1571 CTGAGAGAACTGAGAACTGAAGAAATCGCGACAGAGAGAG 1615
Db 518 ATGATGAGAGCGAGAGATGATGAAGACGAGAGATGATGAAGACGAGAG 474
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RESULT 13
CA607797/c
LOCUS wr1.pk0082.f4 wr1 Triticum aestivum cDNA clone wr1.pk0082.f4 5'
DEFINITION end, mRNA sequence.
                265 bp mRNA linear EST 21-NOV-2002
REFERENCE Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
AUTHORS Lin, H., van Damme, M., Lavelle, D., Chevallier, P., Ziegler, J.,
Ellison, P., Kolkmann, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
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ACCESSION CA607797
VERSION CA607797.1 GI:25162959
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Poideae; Triticeae; Triticum.
JOURNAL 1 (bases 1 to 265)
COMMENT Tingley, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.
Unpublished (2002)
Contact: Scott V. Tingley
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingley@USA.dupont.com
Seq primer: M13.
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ORIGIN
Query Match 4.5%; Score 98.4; DB 14; Length 265;
Best Local Similarity 62.7%; Pred. No. 7e-10;
Matches 141; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 1391 AGGATGAGAGGATTCGACATTGATATCGCGAAGAGGAGCGAGACGAAATTCGGAAG 1450
Db 240 AAGATGATGTTGAAGTGCAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATG 181

Qy 1451 ATGATACCGCGAGAGTGAAGTCCGAGAGAGGAGAGCTGAAGAACCGAGAGAGAAA 1510
Db 180 AAGAAGATGAAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121

Qy 1511 CTGATGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
Db 120 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 61

Qy 1571 CTGAGAGAACTGAAGAAATCGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
Db 60 ANGAAGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 16
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RESULT 14
BU005139/c
LOCUS QG7D20.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
DEFINITION QG7D20, mRNA sequence.
ACCESSION BU005139
VERSION BU005139.1 GI:22439534
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
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REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
TITLE 1 (bases 1 to 263)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevallier, P., Ziegler, J.,
Ellison, P., Kolkmann, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
```

Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
singleton, see http://cpdb.ucdavis.edu/ for details.
Plate: QGS7 row: D column: 20.

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: M column: 07
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 689.

FEATURES
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/db_xref="taxon:10090"
/clone="UUC2M0245M07"
/sex="Female"
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/clone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 4.5%; Score 97.6; DB 28; Length 689;
Best Local Similarity 59.3%; Pred. No. 1.1e-09;
Matches 166; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
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Db 2 TGNATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
QY 1400 AGGATTCGACATTGATATGGCGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1459
Db 62 AGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121
QY 1460 GCGAAGTGAAGTTCACCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1519
Db 122 AGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
QY 1520 ACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1579
Db 182 AGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
QY 1580 CTGAAGAACTGAAGAAATCCCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1619
Db 242 AAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 281

Search completed: August 25, 2004, 05:21:07
Job time : 4954.35 secs

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Class: plasmid ends
High quality sequence stop: 689.

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ORIGIN
Query Match 4.5%; Score 97.8; DB 13; Length 263;
Best Local Similarity 63.3%; Pred. No. 9.4e-10;
Matches 150; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
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Db 263 AACAGACAGAAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 204
QY 1439 AAATTTCCGAAGATGATACGGCGAAGTGAAGTCAACCGAAGAGGAGGAGGAGGAGGAG 1498
Db 203 AAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 144
QY 1499 CCGAAGAGAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1558
Db 143 AAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 84
QY 1559 AAAGTGAAGAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1615
Db 83 AAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 27

RESULT 15
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LOCUS 689 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0245M07R Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0245M07 R, genomic survey sequence.
ACCESSION AZ971991
VERSION 1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 689)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Kelly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 23:48:06 ; Search time 1091.79 Seconds
(without alignments)
9777.159 Million cell updates/sec

Title: US-10-735-098-3
Perfect score: 2169
Sequence: 1 atgtgtaacgaattatgg.....tcagaggagtggaataatga 2169

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2169	100.0	2169	17	US-10-735-098-3
2	162.4	72.0	2124	17	US-10-735-098-9
3	1454.2	67.0	2226	13	US-10-882-172A-29815
4	1375.8	63.4	2326	17	US-10-735-098-5
5	1304.8	60.2	2277	17	US-10-735-098-1
6	1250.6	57.7	2262	17	US-10-735-098-7
7	439.2	20.2	1000	17	US-10-343-561-15
8	97	4.5	31124	13	US-10-087-192-463
9	95.2	4.4	635	13	US-10-027-632-269927
10	95.2	4.4	635	16	US-10-027-632-269927
11	91.8	4.2	554	14	US-10-101-487-69
12	91.4	4.2	522	14	US-10-101-487-71
13	91.4	4.2	530	14	US-10-101-487-73
14	91.4	4.2	554	14	US-10-101-487-106

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c 16	89.8	4.1	305	9	US-09-864-761-19262
c 17	89.8	4.1	37265	13	US-10-087-192-49
c 18	89.6	4.1	276	9	US-09-864-761-20595
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c 20	85.8	4.0	1032	16	US-10-369-493-26107
c 21	85.4	3.9	929	13	US-10-294-934-14
c 22	85.4	3.9	96596	12	US-10-052-482-15
c 23	84.8	3.9	143899	10	US-09-972-546-15
c 24	84.6	3.9	39443	16	US-10-085-117-313
c 25	83.2	3.8	1001	13	US-10-294-934-439
c 26	82.8	3.8	374849	13	US-10-087-192-1627
c 27	82.2	3.8	3300	17	US-10-467-534-80
c 28	82.2	3.8	193853	13	US-10-087-192-1663
c 29	81.6	3.8	54786	12	US-10-052-482-211
c 30	81	3.7	96602	16	US-10-085-117-61
c 31	80.8	3.7	462	9	US-09-864-761-3829
c 32	80.6	3.7	106664	15	US-10-175-523-97
c 33	80.6	3.7	115223	17	US-10-322-281-773
c 34	80.4	3.7	122859	13	US-10-087-192-37
c 35	79.8	3.7	138115	17	US-10-322-281-377
c 36	79	3.6	45980	10	US-09-957-956-6
c 37	78.8	3.6	286	15	US-10-029-386-18943
c 38	78.8	3.6	577	15	US-10-029-386-5187
c 39	78.4	3.6	315	9	US-09-864-761-21723
c 40	78	3.6	6944	15	US-10-172-086-111
c 41	78	3.6	6944	17	US-10-311-507-113
c 42	78	3.6	48652	13	US-10-087-192-859
c 43	77.8	3.6	536	15	US-10-029-386-19974
c 44	77.8	3.6	599	15	US-10-029-386-6243
c 45	77.6	3.6	438	9	US-09-864-761-4988

ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Petterson-Fernholm, Annika Margareta
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain M98
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2166)
US-10-735-098-3

Query Match 100.0%; Score 2169; DB 17; Length 2169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTAACCGAATTATGCGCGCATCTGTTGTCCTTACTTTGGCATCTTGCATC 60
Db 1 ATGTGTAACCGAATTATGCGCGCATCTGTTGTCCTTACTTTGGCATCTTGCATC 60

QY 61 GCGGCAATTTCCGCGTGCAGCTGTTGTCGAATCAACGCCGACCGCGTACCCCGTCACT 120
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QY 121 TTCAAGTCTAAGAGGTTCCCACTTCGCCCTCCCGGCTCTCGGTAGAAACACGCGC 180
Db 121 TTCAAGTCTAAGAGGTTCCCACTTCGCCCTCCCGGCTCTCGGTAGAAACACGCGC 180
QY 181 GTCAACACGCGCGTCCGTCGCGCAATGCGGTGTTGAGACGGAATPACTGCTTTTCAT 240
Db 181 GTCAACACGCGCGTCCGTCGCGCAATGCGGTGTTGAGACGGAATPACTGCTTTTCAT 240
QY 241 CGTGAAGTGCACGGCAATTTCCGATAGCAAAACAGCAGAGAAAGCTGCTGTTTAAA 300
Db 241 CGTGAAGTGCACGGCAATTTCCGATAGCAAAACAGCAGAGAAAGCTGCTGTTTAAA 300
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Db 421 TATAATTTATCGGTTGTCAGTCCCGTTATGTTGTTTACTAAAAACGGAAGATGAATTT 480
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Db 541 TATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGAAACGGTGAAATPATTCCGCG 600
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Db 601 AACTGGCAATATGACCGATGCCATAGTATCGGAGAGGTAAGGGGTTTCCAGTGTG 660
QY 661 GATTTGGGTTATACACATPATTATGTAATGAAATGGGCGAGCTTCTTATGAGGCTAG 720
Db 661 GATTTGGGTTATACACATPATTATGTAATGAAATGGGCGAGCTTCTTATGAGGCTAG 720
QY 721 GATGCGGATGCGCGGAAACATCTCGCGCAATATACGGTTAAATTCGACAAAAAAAC 780
Db 721 GATGCGGATGCGCGGAAACATCTCGCGCAATATACGGTTAAATTCGACAAAAAAAC 780
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Db 781 CTGGAAGGTAAGTTGATTAATAATCAGTATGTCRAAAGAGAGATGATCCTTAAATCCA 840
QY 841 CTGACCATTTACAAATACCGCAATTTGGACGCAACCGCTTTTACCGGCGAGTGCCTAA 900
Db 841 CTGACCATTTACAAATACCGCAATTTGGACGCAACCGCTTTTACCGGCGAGTGCCTAA 900
QY 901 GTTAGCACCGAGTGAAGACGCAACACGCTGATTAAGAAATATTTGTTTTCATACCGAT 960
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QY 961 GCGGATCAGGGCTTACGGCGGTTTTCGGCGATAACGGAAGAGCTTGCAGGCGG 1020
Db 961 GCGGATCAGGGCTTACGGCGGTTTTCGGCGATAACGGAAGAGCTTGCAGGCGG 1020
QY 1021 TTTATCAGTAACGACAAACGCTTATTCGGCGTTCGCGGCAAAACAAAAACAGAGACA 1080
Db 1021 TTTATCAGTAACGACAAACGCTTATTCGGCGTTCGCGGCAAAACAAAAACAGAGACA 1080
QY 1081 GCAACCGCATCAGATCAAAATCTGCGCTGCGGCTGCGGAAACACACCAAAATCTTGGAT 1140
Db 1081 GCAACCGCATCAGATCAAAATCTGCGCTGCGGCTGCGGAAACACACCAAAATCTTGGAT 1140

QY 1141 TCTCTAAAAATTTCCGTTGACGAGCGGACCTGATGACCATGCCCGTAAGTTTTCGCAATTTC 1200
Db 1141 TCTCTAAAAATTTCCGTTGACGAGCGGACCTGATGACCATGCCCGTAAGTTTTCGCAATTTC 1200
QY 1201 ACTATGCCGATTTTGGTTCATCCCGACAAATCTTGTGTAAGGGCGGTGAAATTCCTTTG 1260
Db 1201 ACTATGCCGATTTTGGTTCATCCCGACAAATCTTGTGTAAGGGCGGTGAAATTCCTTTG 1260
QY 1261 GTTAGCCAGAGAAACCATCGAGCTTGCAGCGGAGGAAATGACCATCCGCTGCTTGT 1320
Db 1261 GTTAGCCAGAGAAACCATCGAGCTTGCAGCGGAGGAAATGACCATCCGCTGCTTGT 1320
QY 1321 TGCGATTTCTGACCTATGTGAAACTCGGACGGATAAAAAACCGACCGCGCGCTCAAA 1380
Db 1321 TGCGATTTCTGACCTATGTGAAACTCGGACGGATAAAAAACCGACCGCGCGCTCAAA 1380
QY 1381 CCGAAGCGCAGGATGAAGAGATTGCGACATTTGATTAATGCGGAAGAAAGCGAGACGAA 1440
Db 1381 CCGAAGCGCAGGATGAAGAGATTGCGACATTTGATTAATGCGGAAGAAAGCGAGACGAA 1440
QY 1441 ATTTCCGAAGATGATTAACGGCGAAGATGAAGTCAACCGAAGAGAGGAAAGCTGAAGAAC 1500
Db 1441 ATTTCCGAAGATGATTAACGGCGAAGATGAAGTCAACCGAAGAGAGGAAAGCTGAAGAAC 1500
QY 1501 GAAGAAGAAACTGTATGAAGACGAAGAGAAACCCGGAAGAACTGAAGAACTGAAGAA 1560
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QY 1561 ACTGAAGAAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA 1620
Db 1561 ACTGAAGAAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA 1620
QY 1621 GCGGTTCCAGCGCATCTCCCACTCCGGAAGCTCTTAAAGCGAGGACATCGACCTT 1680
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QY 1681 TTCTCTGAAAGTATCCGCAACCGGAGCGGACATTCGCAAAATTTGGAAGACGCTAT 1740
Db 1681 TTCTCTGAAAGTATCCGCAACCGGAGCGGACATTCGCAAAATTTGGAAGACGCTAT 1740
QY 1741 ACCGCGACTTGGGAAGCGGTATCGCGTTCGGATTAAGAGGCGGAAACAGCTAGTGC 1800
Db 1741 ACCGCGACTTGGGAAGCGGTATCGCGTTCGGATTAAGAGGCGGAAACAGCTAGTGC 1800
QY 1801 ACTAGCTCATTTCAAAAGGATAGCTATGCGAATCAAGCGGCAAAAGCGAATTTGACGTT 1860
Db 1801 ACTAGCTCATTTCAAAAGGATAGCTATGCGAATCAAGCGGCAAAAGCGAATTTGACGTT 1860
QY 1861 GATTTTGTGCGAAGTCTGTTTTCGCGCAAGGTTGCGAATTAATCCCAAGTTTAAAGCCAGT 1920
Db 1861 GATTTTGTGCGAAGTCTGTTTTCGCGCAAGGTTGCGAATTAATCCCAAGTTTAAAGCCAGT 1920
QY 1921 TTTTATTTGAAAAAGGTTGATTCATGCGAAGGTTTCCAGCTTTCGCGGCTACTCGT 1980
Db 1921 TTTTATTTGAAAAAGGTTGATTCATGCGAAGGTTTTCAGCTTTCGCGGCTACTCGT 1980
QY 1981 GAAATGTTGTTGATTTGTTCTGCGCAAGGTTGCGAATTAATCCCAAGTTTAAAGCCAGT 2040
Db 1981 GAAATGTTGTTGATTTGTTCTGCGCAAGGTTGCGAATTAATCCCAAGTTTAAAGCCAGT 2040
QY 2041 AATCTTCTCGTAGAAGGAGATTTTATGTCGCGAGCGGAGAGTTGGTGGTATATTT 2100
Db 2041 AATCTTCTCGTAGAAGGAGATTTTATGTCGCGAGCGGAGAGTTGGTGGTATATTT 2100
QY 2101 ATCGACAGTGCAGGAAATCGCGGTTGTTTCGGTGCGAAGAAAGATATGAGAGAGGTG 2160
Db 2101 ATCGACAGTGCAGGAAATCGCGGTTGTTTCGGTGCGAAGAAAGATATGAGAGAGGTG 2160
QY 2161 GAAAAATGA 2169
Db 2161 GAAAAATGA 2169

RESULT 2

```

US-10-735-098-9
; Sequence 9, Application US/10735098
; Publication NO. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735, 098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain 881607
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2121)
US-10-735-098-9

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Query Match	72.0%;	Score 1562.4;	DB 17;	Length 2124;
Best Local Similarity	84.5%;	Pred. No. 0;		
Matches 1835;	Conservative 0;	Mismatches 286;	Indels 51;	Gaps 5;
QY	1	ATGTGTAACCGCAATATGCGGCATTTGTCCTTGTTCGCCCTTACCTTTTGGCAATCTTGCAATC	60	
Db	1	ATGTGTAACCGCAATATGCGGCATTTGTCCTTGTTCGCCCTTACCTTTTGGCAATCTTGCAATC	60	
QY	61	GGCGGCAATTTCCGCGTGCAGCCCTGTTTGCAGATCAACGCGCAGCCGGTACCCCGTCACT	120	
Db	61	GGCGGCAATTTCCGCGTGCAGCCCTGTTTGCAGATCAACGCGCAGCCGGTACCCCGTCACT	120	
QY	121	TTCAAGTCTAAGGACGTTTCCCACTTCGCCCCCTCCCGGGTCTTCGGTAGAAGCAACGCGC	180	
Db	121	TTCAAGTCTAAGGACGTTTCCCACTTCGCCCTCTCCCGGGTCTTCGGTAGAAGCAACGCGC	180	
QY	181	GTCAACAGCCCGCGTGCAGTTCGGGCAATGCGGCTGTGTAGACGGAATCTGCTTTTCAT	240	
Db	181	GTCAACAGCCCGCGTGTGTGGGCAATGCGGCTGTGTAGACGGAATCTGCACTTCT	240	
QY	241	CGTGAAGATGGCAGCGCAATTCGCGATAGCAACCAAGCAGAGAAAAGCTGTCGTTTAAA	300	
Db	241	GATPAGATGGCAATGATTTTCCAAATAGCAACCAAGCAGAGAAAAGCTGTCGTTTAAA	300	
QY	301	GAAGGTGATGTTCTGTTTTTATACGGTTCACAAAGAAAATAAACTTCAACAACCTTTAAAGC	360	
Db	301	GAGCAAGATATCTGTTTTTATACGGTTCACAAAGATCAAGTCAAGAGCTTTAAAGAT	360	
QY	361	GAAATTCATAAAGCTAATCTCTGAGGCAAGATTTACCATCGGAAATGAAAAATAAAAA	420	
Db	361	AAATTTGCTCAACCAAAATCTACGGCAAGATTTACCAATCGGAAAGAAAATAAAAA	420	
QY	421	TATAATTTATCGGTTTTGTCACTGCGGGTTATGTGTTTACTAAAAACGGAAAGATGAAAT	480	
Db	421	TATGATTTATAAATTTGTAGATGCAGTTATGTTATATATTAAGACGGAAAGATGAAAT	480	
QY	481	GAGAAACATTCGGATGAAAGACAGTTTTCTPAATCGTTTTAGGCTATACGCGTTTGTATAT	540	
Db	481	GAGTGGACTTTCAAATTTACAGCAGTCTACCAACCGGTTTGGTTTATGACGGTTTGTATAT	540	
QY	541	TATCTCGGAGAACATCCTTCCCAATCTTTTACCGCGCGGGAACGCTGAAATTTTCCGGC	600	
Db	541	TATTCGGAGAACATCCTTCGCAATTTTACCGCGCGGGAACGCTGAAATTTTCCGGC	600	

QY	601	AACTGCAATATATAGACCGATCCCATACGTATCGAGAGGTAA---GGGGGTTCCTCAGT	657
DB	601	AACTGGCAATATATGACCGGATGCCATACGTATCGAAACAGGAAACGACGAGATCCTAGC	660
QY	658	GTGGATTTGGGTATATACACATATTATGGTATAGAAAATTTGGGGCAGCTTCTTATGAGGCT	717
DB	661	GAAGATTTGGGTATATCGTTTATTCGCTCAAAATGTTCGAGCAACTTCTTATGCTGGCG	720
QY	718	AGGGATGCCGATGGCGCGGAAAAACATCTCTGCCGATATACGGTTTAATTTTCGACAAAAA	777
DB	721	ACTGCCGACGACCGGGAGGGAACATCTCTGCCGAATATACGGTTAATTTTGACCAAAAA	780
QY	778	AACCTGGAAGGTAAAGTTGATTAAAAATCAGTATGTGCAAAACAGAGATGATCCTAAAAAT	837
DB	781	ACTCTGAATGGCAAGCTGATTAAAAATCAGTATGTGCAAAAGAGAGATGATCCTTAAAAA	840
QY	838	CCACTGACCATTTACAAATTTACCGCAATTTGACGGCAACCGCTTTTACCGGACGTGCC	897
DB	841	CCACTGACCATTTACGACATTTACTGCAAAATTTGACGGCAACCGCTTTTACCGGACGTGCC	900
QY	898	AAAGTTAGCACCGAGGTGAACACGCAACGCTGATAAAGAAATATTTCTTTTCCCATACC	957
DB	901	AAAGTTTACACAGAGGTGAAGAGATCACGCTGATAAAGAAATATTTGTTTTCCATACC	960
QY	958	GATGCCGATCAGCGGCTTTGAGGCGGTTTTTTCGGCGATAACGGAGAGAGCTTGCCGGG	1017
DB	961	GATGCCGATCAGCGGCTTTGAGGCGGTTTTTTCGGCGATAGGGGAGAGCTTGCCGGA	1020
QY	1018	CGGTTTATCAGTAAAGCAACAGCGTATTTCGGCGTGTTCGAGGCAACAAAAACAGAG	1077
DB	1021	CGGTTTATCAGCAACAGCAACAGCGGTATTTCGGCGTGTTCGAGGCAACAAAAACAGAG	1080
QY	1078	ACAGCAAAACGATCAGATACAAATCTTCGCCCTCGCGTCTGAAACACACCAAAATCTTG	1137
DB	1081	ACAGCAACGATCAGATACAAATCTTCGCCCTCGCGTCTGAAACACACCAAAATCTTG	1140
QY	1138	GATTCTCTAAAAATTTCCGTTGACGAGCGCATGATGACCATGCCCTTAAGTTTGCCATT	1197
DB	1141	GATTCTCTAAAAATTTCCGTTGACGAGCGCAAGTGTGAANAATCCCCACGTTTGAGTT	1200
QY	1198	TCCACTATGCCGATTTTGTGTATCCCGACAACATTTCTGTGAAAGGCGTGAATTCCT	1257
DB	1201	TCCACTATGCCGATTTTGTGTATCCCGACAACATTTCTGTGAAAGGCGTGAATTCCT	1260
QY	1258	TTGTTTAGCCAAAGAAAAACCATCGAGCTTCCGACGGCAGGAAATGACCATCCGTGCT	1317
DB	1261	TTGTTTAAACAAAGAACCAACATCGATCTTTCCGACGGCAGGAAATGACCGTCCGTGCT	1320
QY	1318	TGTTGCGATTTTCTGACTTATGTGAAACTCGGACGGATAAAAAACCGACCCCGCGCGTC	1377
DB	1321	TGTTGCGACTTTTGTACCTATGTGAAACTCGGACGGATAAAAACCGAACGCCCGCGCTC	1380
QY	1378	AAACCGAAGCGCAGGATGAGAGGATTCGGACATTTGATTAATGGCGAAGAACGCAAGAC	1437
DB	1381	CAACCGAAGCGCAGGATGAGAGGAGGGAACGAAAGGGTGTAGCGCTTGATACCGGTAAA	1440
QY	1438	GAATTTTCCGAAGATGATTAACGCGCAAGATGAAGTCACCGAAGAGAGGAGCTGAAGAA	1497
DB	1441	GAAG---GCGAAGACGAATTCGCGATGAAGAAGCACC GGAGA-----1481	
QY	1498	ACCGAAGAGAAACTGATGAAGACGAGAGGAGAAACCCGAGAAAACTGAAGAACTGAA	1557
DB	1482	--CGAAGTCGTAGAAGATGAAGACGAAGATGAAGACGAAGAGAAATCGAA-----GAA	1533
QY	1558	GAAACTGAAGAACTGAAGAACTGAAGAAATGTAAGAAAAATTCGCCGACAGAAGAGGC	1617
DB	1534	GAACCTTGAAGAAAGACTGAAGAGGAGAAACCGAAGAGAAATTTGCCGCGACGAAGGC	1593
QY	1618	AACGGCGGTTTCAGGACAGCATCTGCCCATCTCCGGAAGCTCTAAGGCHAGGACATCGAC	1677
DB	1594	AACGGCGGTTTCAGGACAGCATCTGCCCATCTCCGGAAGCTCTAAGGCHAGGACATCGAC	1653

QY 1678 CTTTCTCTGAAGTATCCACCGGGAAGCCGACATTCGGCAATTCGAAAGCAGC 1737
 Db 1654 CTTTCTCTGAAGTATCCACCGGGAAGCCGACATTCGAAAGCAGC 1713
 QY 1738 TATACCGGCACTTGGGAAGCGGTATCGGCGTGCCTGATAGAAAGCGCAAGCTAGAT 1797
 Db 1714 TATACCGGCACTTGGGAAGCGGTATCGGCGTGCCTGATAGAAAGCGCAAGCTAGAT 1753
 QY 1798 GGCACCTACGTCCTATCAAAAGGATAGCTATCGCAATCAAGCGGCAAAAGCAGAAATTTGAC 1857
 Db 1754 -GTGGTACGTCCTATCAAAAGGATAGCTATCGCAATCAAGCGGCAAAAGCAGAAATTTACC 1812
 QY 1858 GTTGATTTTGGTGGAGTGCCTTTCAGTAAAGTTGACAGAAAGGATGATACACACCC 1917
 Db 1813 GTTGATTTTGGAGGAGAGCGGTGTCGGGAATGCTGACAGAAAGGATGATACACACCC 1872
 QY 1918 GCTTTTATATGAAAAAGGTGATGATGATGCGCAACGCTTTCCACGCTTTGGCGCGTACT 1977
 Db 1873 GCTTTTATATGAAAAAGGTGATGATGATGCGTAAACGCTTTCCACGCTTTGGCGCATACT 1932
 QY 1978 CGTGAATAGGTGTTGATTTGCTGGGCAAGTTTCGACTAATCCCAAGTTTAAAGCC 2037
 Db 1933 CGGAGAAACGCTATTTGACCTTTCTGGGCGAGGTTTCGACTAACCCGAAAGACTTCAAAGCC 1992
 QY 2038 AGTAATCTTCTGTAAGAGGATTTTATGCTCGCAGCGGCGAGGTTGGGTGTAAT 2097
 Db 1993 GACAATCTTCTGTAAGAGGATTTTATGCTCGCAGCGGCGAGGTTGGGTGTAAT 2052
 QY 2098 ATTATCGACAGTGCAGGAAATCGGCGTGTGATTTGGTGCAGAAAGATATGACGAG 2157
 Db 2053 ATTATCGACAGTGCAGGAAATCGGCGTGTGATTTGGTGCAGAAAGATATGACGAG 2112
 QY 2158 GTGGAATAATCA 2169
 Db 2113 GCAACACGATGA 2124

RESULT 3
 US-10-282-122A-29815
 ; Sequence 29815, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELTRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 29815
 ; LENGTH: 2226
 ; TYPE: DNA
 ; ORGANISM: Neisseria meningitidis
 ; US-10-282-122A-29815
 Query Match 67.08; Score 1454.2; DB 13; Length 2226;
 Best Local Similarity 81.98; Pred. No. 0;
 Matches 1742; Conservative 0; Mismatches 343; Indels 42; Gaps 4;
 QY 1 ATGTGTAACCGCAATTAATGGCGCATTTGTCTTGTGTGCTTCTTTTGGCATCTTGGCATC 60
 Db 1 ATGTGTAACCGCAATTAATGGCGCATTTGTCTTGTGTGCTTCTTTTGGCATCTTGGCATC 60
 QY 61 GCGCGCAATTTTGGCGGTGCGACCTTGTGTCGAATCAACGCGCAGCGGTACCCGCTCACT 120
 Db 61 GCGCGCAATTTTGGCGGTGCGACCTTGTGTCGAATCAACGCGCAGCGGTACCCGCTCACT 120
 QY 121 TTCAAGTCTAAGGACGTTTCCACATTCGCCCTTCCGGTCTTCGGTAGAAACCAACGCGC 180
 Db 121 TTCAAGTCTAAGGACGTTTCCACATTCGCCCTTCCGGTCTTCGGTAGAAACCAACGCGC 180
 QY 181 GTCAACGAGCCGCGCTGCGTGGCGCAATGCGGTGTGTGAGACGGAATACCTTTTTCAT 240
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 QY 421 TATATATATCGGTTTGTGTCAGTCCGCTTATGTTTACTTAAACGAGAAAGATGAAAT 480
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QY 838 CCACTGACCAATTACCAACATTACCGCAACATTCGACGGCAACCGCTTTACCGGAGTGCC 897
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QY 841 CCGCTGACCAATTACGACATTACTGCAACATTGAGCGCAACCGCTTTACCGGAGTGCC 900
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QY 898 AAGTTAGCACCGAGGTGAGAGCAACACGCTGATAAAGAAATTTGTTTTTCCATACC 957
Db |||||
QY 901 AAGTTAAACACCGAGGTGAGAGCAACACGCTGATAGAGAGATTGTTTTTCCATACC 960
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QY 958 GATCGCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCGATAACCGAAGAGCTTGCGGG 1017
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QY 961 GATCGCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCGATAACCGAAGAGCTTGCGGG 1020
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QY 1078 ACAGCAACCGATCAGATCAAAATCCTGCCCTGCGCTGCGAACAACACCAAAATCTTG 1137
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QY 1081 GCATCAACCGCATCAGATCAAAATCCTGCCCTGCGCTGCGAACAACACCAAAATCTTG 1140
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QY 1138 GATTCCTTAAATTTCCGTTGACGAGGCACTGATGACATGCCGCTAAGTTTGCAAT 1197
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QY 1141 GATTCCTTAAATTTCCGTTGACGAGGCACTGATGACATGCCGCTAAGTTTGCAAT 1200
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QY 1198 TCCACTATGCCGATTTTGGTTCATCCCGCAAACTTCTTGTGAGAGGCGTGAATTCCT 1257
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QY 1201 TCCCTATGCCGATTTTGGTTCATCCCGCAAACTTCTTGTGAGAGGCGTGAATTCCT 1260
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QY 1258 TTGGTTAGCAAGAGAAACCAATCAGCTTTCGCGAGCGGAGAAATGACCATCGTGCT 1317
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QY 1261 TTGCTCAAGATACCTCAAAACATCGATCTTTCGCGAGCGGAGAAATGACCGTCACTGCT 1320
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QY 1318 TGTTCGATTTTCACTATGTGAACTCGAGCGGATAAAACCGAAGCGGCGGCGCTC 1377
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QY 1321 TGTTCGATTTTCACTATGTGAACTCGAGCGGATAAAACCGAAGCGGCGGCGCTC 1380
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QY 1378 AAACCGAAGGCGAGATTAAGA---GGATTCGAGATTTGATTAATGCGGAGAAAGCA 1434
Db |||||
QY 1381 AAACCGAAGGCGAGATTAAGA---GGATTCGAGATTTGATTAATGCGGAGAAAGCA 1440
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QY 1435 GACGA---AATTTCCAGAGATGATAACCGCGAAGATGAAGTCAACCGAAGAGAGAGCT 1491
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QY 1441 GAGGATTTGGTTCGCTGAAGAGAAACACCGAAGAGAGTCTGTAAGAGATGAAGACAGA 1500
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QY 1492 GAAGAAACCGAGAGAACTGATGACAGAGAGAGAGAACCCGAGAGAACTGAAGAA 1551
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QY 1501 GAAGAAACCGAGAGTTTCCGAGAGATGGTAACTGAGAGAGAGAGAAATCGCCGAGAA 1560
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QY 1552 ACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAAATCGCCGAGAA 1611
Db |||||
QY 1561 GATGATGATGAAGCGGAGAGAGAGTTGAGAGAACCGAGAGAGATCGCCGAGAA 1620
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QY 1612 GAAGCGAACCGGCTTGAGGAGATCTGCGCACTCGGAGAGCTCTAAAGGAGAGGAC 1671
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QY 1621 GCGCGGCTGCGGCTTGAGAGAGATCGCGGCTCGGAGAGCTCTAAAGGAGAGGAC 1680
Db |||||
QY 1672 ATCGACCTTTTCTGAAAGGTATCGGACGCGAGAGCGGATTCGCAATTTGAGAAA 1731
Db |||||
QY 1681 ATCGACCTTTTCTGAAAGGTATCGGACGCGAGAGCGGATTCGCAATTTGAGAAA 1740
Db |||||
QY 1732 GCACGCTATACCGGCACTTGGAGAGCGGATTCGCGGCTGCGGATGAAGAGGAGACAG 1791
Db |||||
QY 1741 GCACGCTATACCGGCACTTGGAGAGCGGATTCGCGGCTGCGGATGAAGAGGAGACAG 1800
Db |||||
QY 1792 CTAGATGGCACTACGCTCAATTCAGAGGATAGCTATGCAATCAAGCGGCAAGAGAGAA 1851
Db |||||
QY 1852 TTTGACGCTGATTTTGGTGGAGTTCGCTTTGAGTGAAGTTGACAGAAAAAATGATACA 1911
Db |||||
QY 1828 TTTGACGCTGATTTTGGTGGAGTTCGCTTTCCGAGACGCTGACCGGAGAAAAACGGTGT 1887
Db |||||

QY 1912 CACCCCGCTTTTATATTGAAAAAGGTGTGATTGATGGCAACGGTTTCCACGCTTTGGCG 1971
Db |||||
QY 1888 GAAGCTGCTTTCTATATTGAAAAAGGTGTGATTGATGGCAACGGTTTCCACGCGACAGA 1947
Db |||||
QY 1972 CGTACTCGTGAATAAGTGTGATTGCTGGCAAGGTTTCACTAATCCCAAGTTTTT 2031
Db |||||
QY 1948 CGCACTCGGAGTAACGGCATCAATCTTTCGGGAATGGTTTCGACCAACCCCAACCTTC 2007
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QY 2032 AAAGCCAGTAATCTTCTCGTAGAAGAGGATTTTATGTCCTCGGAGGCGGAGAGTTGGGT 2091
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QY 2008 CAAGCTAGTGAATCTTCTGTGAGAGAGGATTTTACGGGCCCGCAGCGGAGGATTTGGGC 2067
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QY 2092 GGTAAATATTATCGACAGTGCACCGGAAA 2118
Db |||||
QY 2068 GGTACTATTATTTCAATAAGGATGGAAA 2094
Db |||||

RESULT 4

US-10-735-098-5
; Sequence 5, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10735,098
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain H44/76
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2223)
US-10-735-098-5

Query Match 63.4%; Score 1375.8; DB 17; Length 2226;
Best Local Similarity 80.4%; Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 357; Indels 60; Gaps 6;

QY 1 ATGTGTAACCGAATTATGGCGCATGCTGTGTCCTTACTTTGGCATCTTGCATC 60
Db 1 ATGTGTAACCGAATTATGGCGCATGCTGTGTCCTTACTTTGGCATCTTGCATC 60
QY 61 GGGCGCAATTTCGCGGTGAGCGCTTGTGCAATCAACGCGGCTACCCCGTCACT 120
Db 61 GGGCGCAATTTCGCGGTGAGCGCTTGTGCAATCAACGCGGCTACCCCGTCACT 120
QY 121 TTCAGTCTAAGAGCGTTCCCACTTCGCCCTCGCGGTCTTTCGGTAGAAACCCACGCG 180
Db 121 TTCAGTCTAAGAGCGTTCCCACTTCGCCCTCGCGGTCTTTCGGTAGAAACCCACGCG 180
QY 181 GT-----CAACCAAGCGCGCTCGGTGCGGCAATCGGCTGTGAGACGGAATCTGCT 234
Db 181 GTCCCGTCAACCGGCGCTCGGTGCGGCAATCGGCTGTGAGACGGAATCTGCT 240
QY 235 TTTTCATCGTGAAGATGCGACGCAATTTCCCGATAGCAAAACAGCAGAGAAAGCTGTCG 294
Db 241 ACTTCTGATAAGGTGCGCAATGATTTTCCAAATAGCAACAGCAGAGAAAGCTGTCG 300
QY 295 TTTAAAGAGGTGATGTTCTGTTTTTATACGGTTTCAAAAAGAAATAAATCTTCAACAATT 354
Db |||||

Db	301	TTTAAAGAAAGGTGATGTTCTGTTTTTATACGTTCAAAAAGATATAAATCTTCAGTGGCTT	360
QY	355	AAAAGCGAAATTCATAACGTAATCTCTGAGGCAAGCAATTCACCATCGAAAATCAAAAT	414
Db	361	AAGGATTAATTCATCAACGCAATCTTAATCTAGAAATTAGGACATCAGAAAATGAAAT	420
QY	415	AAAAAATAAATATTCGGTTTGTGACGTCGGTGTATGTTGTTTCTAATAAACCGAAAGAT	474
Db	421	AAAAAATAATGTTATGAAATTTGTGATCCGGTTATGTTATATATCTTAAAAAACGGAACAGAT	480
QY	475	GAAATTCGAAAACATCGGATGAAAGCAGTTTCTAATCTGTTTAGGCTATGACGGTTT	534
Db	481	GAAATTCGAGTGGACTTCAAAATCGCAAGCAGTTTCTAATCTGTTTAGGCTATGACGGTTT	540
QY	535	GTATATATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGCGGAAACGGTGAATAT	594
Db	541	GTATATATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGCGGAAACGGTGAATAT	600
QY	595	TCCGGCAATCGCAATATGACCGATGCGCATACGTATCGGAGAGTAA---GGGGT	651
Db	601	TCCGGTAACTGGCAATATATGACCGATGCGCATACGTATCGGAGAGTAA---GGGGT	660
QY	652	TCCAGTGTGGATTCGGTTTATACCAATATATGTTAATGAAATTCGGGACGCTTCTTAT	711
Db	661	CCTAGCGAAGATTTGGGTTATCTGTTTATACGTTCAAAATGTCGGACAACTTCTTAT	720
QY	712	GAGGCTAGGGATGCGGATGCGCGGAAACATCTCGCGGAATATACGTTTAAATTCGAC	771
Db	721	GCTGCGACTGCGGACGCGCGGAGGAAACATCTCGCGGAATATACGTTTAAATTCGAT	780
QY	772	AAAAAAACCTGGAGTAAAGTTGATTAATAATCAGTATGTCGCAAGAGAGATGATCT	831
Db	781	AAGAAACATCTTCACGGGTTCAATTAATTAATAATCAGTATGTCGCAAGAGAGATGATCT	840
QY	832	AAAAATCCACTGACATTTCAACATTCACGCAACATTCGAGCGCAACCGCTTTTACCGG	891
Db	841	AAGAAACCTGACATTTACGACATTCGCAACATTCGAGCGCAACCGCTTTTACCGG	900
QY	892	AGTGCCAAAGTTAGCACCGAGGTGAAGACGCAACAGCTGTATAAGATATTTGTTTTC	951
Db	901	AGTGCCAAAGTTAAACCCGAGTTGAAGACGAGCCAGCTGTATAAGAGCATTTGTTTTC	960
QY	952	CATACCGATGCCGATCAGCGGCTTGAGGGCGTTTTTTCGGCGATACCGAGAGAGCTT	1011
Db	961	CATACCGATGCCGATCAGCGGCTTGAGGGCGTTTTTTCGGCGATACCGAGAGAGCTT	1020
QY	1012	GCCGGCGGTTTATCAGTAACGACAAACAGCGTATTCGGCGTGTTCGACGCAACAA	1071
Db	1021	GCCGGAGGTTTATCAGTAACGACAAACAGCGTATTCGGCGTGTTCGACGCAACAA	1077
QY	1072	ACAGAGACGCAACAGCATCAGATACAAATCTCTGCCCTGCGCTCTGAAAACACACCA	1131
Db	1078	ACAAACGCAACAAACGAGCAGATACAAATCTCTGCTATGCGCTCTGAAAACACACCA	1137
QY	1132	ATCTTGATTTCTTAAATTTCCGTTGACGAGCGCTGATGACCATGCGCTTAAAGTTT	1191
Db	1138	ATCTTGATTTCTTAAATTTCCGTTGACGAGCGCAGATGATGATGCGCTTAAAGTTT	1197
QY	1192	GCCATTTCCACTATGCCGATTTTGGTTCATCCGCAACAACTCTTGTGCAAGGCGGTGA	1251
Db	1198	GCCATTTCCCTCTGCCGATTTTGGCATCCCGCAACAACTCTTGTGCAAGGCGGTGA	1257
QY	1252	ATTCTTTTGTAGCAAGAGAAAACATGACGTTGCCAGCGCAGGAAATGACCATC	1311
Db	1258	ATTCTTTTGTAGCAAGAGAAAACATGACGTTGCCAGCGCAGGAAATGACCATC	1317
QY	1312	CGTCTTTTGTGCAATTTCTGACCTATGTAATCTCGGACGATGATGATGCGCGCC	1371
Db	1318	CGTCTTTTGTGCAATTTCTGACCTATGTAATCTCGGACGATGATGATGCGCGCC	1377
QY	1372	GCCGTCAAACCGAAGGCGCAGGATGAAGAGATTCGACATTTGATATGCGGAAGAGC	1431
Db	1378	GCAAGTAAACCAAGGCGGAGATGAAGAGATGAAGAGATGAAGAGATGAAGAGATGA	1437

RESULT 5
US-10-735-098-1
; Sequence 1, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2277

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; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain BNCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(2274)
US-10-735-098-1

Query Match
Best Local Similarity 79.1%; Pred. No. 2.2e-307; Length 2277;
Matches 1675; Conservative 0; Mismatches 332; Indels 111; Gaps 6;

QY 1 ATGTGTAAACCGAATTATGCGCGCAATGTCCTGTGTGCGCCCTTACTTTTGGCATCTTGGCATC 60
Db 100 ATGTGTAAACCGAATTATGCGCGCAATGTCCTGTGTGCGCCCTTACTTTTGGCATCTTGTATC 159
QY 61 GCGCGCAATTTCCGGCGTGAGCGCTGTGTGCAATCAAGCCGACCGCGTACCCCGTCACT 120
Db 160 GCGCGCAATTTCCGGCGTGAGCGCTGTGTGCAATCAAGCCGACCGCGTACCCCGTCACT 219
QY 121 TTCAGTCTTAAGGAGCTTCCCACTTCGCCCTCGCGGTCTTCGGTAGAATACCGCGG 180
Db 220 TTCAGTCTTAAGGAGCTTCCCACTTCGCCCTCGCGGTCTTCGGTAGAATACCGCGG 279
QY 181 GTCACACGACCGCGCGTGTGCGCAATGCGGCTGTGTGAGACGGAATACGTCTTTCAT 240
Db 280 GTCACACGACCGCGCGTGTGCGCAATGCGGCTGTGTGAGACGGAATACGTCTTTCAT 339
QY 241 CGTGAAGATGCGACGGCAATTCGCGATAGCAAAACGACGAGAAAGAGCTGTCGTTTAAA 300
Db 340 CGTGAAGATGCGACGGCAATTCGCGATAGCAAAACGACGAGAAAGAGCTGTCGTTTCAA 399
QY 301 GAAGTGATGTTCTGTTTTATACGGTTTCAAAAGAAATAAAGTTCACCACTTAAAGC 360
Db 400 GAAGTGATGTTCTGTTTTATACGGTTTCAAAAGAAATAAAGTTCACCACTTAAAGC 459
QY 361 GAAATTCATAAACGTAATCTGTAGGCAAGCATTAACCATCGGAAATGAAAAATAAAAA 420
Db 460 GAAATTCATAAACGTAATCTGTAGGCAAGCATTAACCATCGGAAATGAAAAATAAAAA 519
QY 421 TATAATATCGTTTGTGTCAGTCCGCGTGTATGTGTTTACTAAAAACGGAAGATGAAAT 480
Db 520 TATAATATATAAATTTGTAGATGCGAGTTATGTAT---ATGTAAAGGGAAGAAATGAAAT 576
QY 481 GAGAAACATCGGATGAAAGCAGTTTCTAATCGTTTGTAGCTATGACGTTTGTATAT 540
Db 577 AAGTGGACTTCAGATTACAGCAGTTTTCACCGCTTAGGTATGACGTTTGTATAT 636
QY 541 TATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGAAACGGTGAATATTTCCGCG 600
Db 637 TATTTCCGGAGAACGTCCTTCCCAATCTTTACCGAGTGGGGAAACGGTGGATATTTCTGGT 696
QY 601 AACTGGCAATATGACCGGATGCCATAGCTATCGGAGAGGTAAAGGGGTTTCCAGTGTG 660
Db 697 AACTGGCAATATGACCGGATGCCAAGCGTATCGAGCAGTAAAGGGGTTTGGCATTGAC 756
QY 661 GATTGGGTTTATCCACATATTATGTAATGTAATTCGAGCGGCAATTTCCGACAAAAAAC 780
Db 757 AATTTGGGTTTATACATTTTATGTAACGATGTTGGTGCAATCTTCTATGCGGCTAAG 816
QY 721 GATGCCGATGCGCGGGAACATCTCTCGCGAATATACGGTTTAATTTCCGACAAAAAAC 780
Db 817 GATGTCGACGAAAGGGAACCAATCTCTGCTAATATACGTAGTTTCGGTACAAAC 876
QY 781 CTCGAGGTTAAGTTGATTAAATCAGTATGTGCAAAAGAGAGATGATCTTAAAAATCCA 840
Db 877 CTCGCGGCGAGCTGATTAAAAACCAATATGTCAACCCAGTGAAGC---AAAAACG 933
QY 841 CTGACCATTTTACAACTTACCGCAACATTCGACGGCAACCGCTTTTACCGCAGTGCATA 900
Db 934 CTGACCATTTTACAACTTACCTGCGATTAAACGCGCAACCGCTTTTACCGCAGTGCATA 993
QY 901 GTTAGCCGAGGTGAAGACGCAACGCTGTATATAAGAAATATTGTTTTCATACCGAT 960
Db 993 GTTAGCCGAGGTGAAGACGCAACGCTGTATATAAGAAATATTGTTTTCATACCGAT 2028
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Db 994 GTCAATCTCTGATTAGCGAAAAGCCATGCAATAGGAGCATTTGTTTTTCCATGCCAT 1053
QY 961 GCCGATCAGCGCTTGAGGCGGTTTTTTTCGGGATAAACGAGAAAGCTTTCGGGCGG 1020
Db 1054 GCCGATCAGCGCTTGAGGCGGTTTTTTTCGGGATAAAGGGGAAAGCTTTCGGACG 1113
QY 1021 TTTATCAGTAAACGACAAACAGCGTATTTCGGCGTGTTCGAGGCAAAACAAAAACAGAGACA 1080
Db 1114 TTTATCAGCAACGACAAACAGCGTATTTCGGTGTATTTCGAGGCAAAACAAAAATAGCC---- 1168
QY 1081 GCAAAAGCATCAGATACAAATCCTGCCCTGCGCTGTGAAAAACACACCAAAATCTTGGAT 1140
Db 1169 -----CCGTGCCCTGTGAAAAACACACCAAAATCTTGGAT 1203
QY 1141 TCTCTAAAAATTTCCGTTGACGAGCGCTGATGACCATGCCCGTAAGTTTCGCATTTCC 1200
Db 1204 TCTCTGAAAAATTTCCGTTGATGAGGCAAGTGGTGAATAATCCCGACCGGTTTCCCATTTCT 1263
QY 1201 ACTATGCCGATTTTGGTCAATCCCGACAAACTTTTGTGGAAGGCGTGAATAATCTTTTG 1260
Db 1264 CCTATGCCGATTTTGGTCAATCCCGACAAACTTTTGTGGAAGGCGATGAATAATCTTTTG 1323
QY 1261 GTTAGCCCAAGAGAAAAACCATCGAGTTTGCAGACGGGAGAAAAATCACCATCGCTGTGT 1320
Db 1324 GTTAGCCCAAGAGAAAAACCATCGAGTTTGCAGACGGGAGAAAAATGACCGTCAGTCTTGT 1383
QY 1321 TCGCATTTTCTGACCTATGTGAAACTCGGACGGATTAATAACCGACCGCCCGCTCAAA 1380
Db 1384 TCGCATTTTCTGACCTATGTGAAACTCGGACGGATTAATAACCGACCGCCCGCTCAAA 1443
QY 1381 CCGAAGCGCAGGATGAAGAGATTTCGACATTTGATATGGCAAGAAAGCGAAGCAAA 1440
Db 1444 CCGAAGCGCAGGACGAGAGATTTCGACATTTGATATGGCAAGAAAGCGAAGCAAA 1503
QY 1441 ATTTCCGAGATGATACGGGCAAGATGAATCAACGGAAGAGAGAGCTGAAGAAACC 1500
Db 1504 ATCGCGATGAGGAAGAGGACCGCAAGATGCAGCGCAGGAGATGAAGCGACGGAAGAA 1563
QY 1501 GAAGAAGAACTGATGAAGACGAGAGAGAAAGCCCGAAGAACTGAAGAACTGAAGAA 1560
Db 1564 GACGAAGCCACAGAAACGAGACGCGCAAGAA----- 1596
QY 1561 ACTGAAGAACTGAAGAACTGAAGAACTGAAGAAATCGCCGACAGAAAGAGCAAC 1620
Db 1597 -----GACGAAGCTGAAGAACTGAAGAAATCGTCG---GCGAAGGCAAC 1641
QY 1621 GCGGTTTCAGGACATCTTCCCATCTCCGAGACCTCTTAAAGCAGGACATCGACCTT 1680
Db 1642 GGCAGTTTCAACCGCATCTTCCCTGTCCGGAAGCTCTTAAAGCAGGATATCGACCTT 1701
QY 1681 TTCTGAAAGGTATCCGACCGCGAAGCGACATTCGCAATTCGCAATTCGAAAGACGCTAT 1740
Db 1702 TTCTGAAAGGTATCCGACCGCGAAGCGAATTAATTTCCGCAAACTGGAGAAGCAGCTAT 1761
QY 1741 ACCGCACTTGGGAAGCGGCTATCGGCTGCCGATTAAGAAAGCGCAACAGCTAGATGGC 1800
Db 1762 ACCGCACTTGGGAAGCGGCTATCGGCAACCCATTCATGAGGACATCATGCGGAT--- 1818
QY 1801 ACTACGTTCATTCAAAAGGATAGTATGGAATCAAGCGGCAAAAGCAGAAATTTGACGTT 1860
Db 1819 -----AAAGAAGCGCAAAAGCAGTATTTCGCTT 1848
QY 1861 GATTTTGTGCGAAGTCCGCTTTTCAGGTAAGTTTCACAGAAATAATGATACACACCGGCT 1920
Db 1849 GATTTGCGCAAGAAATCGATTTCCGGAACGCTGACGAGAAAAACCGGTGTAGAACCTGCT 1908
QY 1921 TTTTATTTGAAAAAGGTCTGATTTGATGCAACCGGTTTCCAGCTTTGCGGCTACTCGT 1980
Db 1909 TTTCCGTTATTGAAAAACCGCGTGTATTGAGGCAACCGTTTCCATGCGGACACGCGCTCGG 1968
QY 1981 GAAATGCGTGTGATTTGTTCTCGGCAAGGTTTCGACTAATTCCTCCCAAGTTTAAAGCCAGT 2040
Db 1969 GATGACGATCGACCTTTCCCGGCGAGGTTTCGACCAACCCGACGATCTTCAAAGCTAT 2028
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Qy	2041	AATCTTCTCGTAGAAGAGGATTTATGTTCCGCGGCGGAGAGTTGGGTGGTAATTT	2100
Db	2029	GATCTTCGTGTAGAAGAGGATTTTACGGCCCGAAGCGGAGGAATTGGGCGGTATTATT	2088
Qy	2101	ATCGACAGTGCAGGAAA	2118
Db	2089	TTCAATAATGATGGGAAA	2106
RESULT 6			
US-10-735-098-7			
; Sequence 7, Application US/10735098			
; Publication No. US20040131634A1			
; GENERAL INFORMATION:			
; APPLICANT: Pettersson-Fernholm, Annika Margareta			
; APPLICANT: Tomassen, Johannes Petrus Maria			
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein			
; FILE REFERENCE: B45106C1			
; CURRENT APPLICATION NUMBER: US/10/735,098			
; CURRENT FILING DATE: 2003-12-12			
; PRIOR APPLICATION NUMBER: 09/485,760			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: PCT/EP98/05117			
; PRIOR FILING DATE: 1998-08-10			
; PRIOR APPLICATION NUMBER: GB 9717423.9			
; PRIOR FILING DATE: 1997-08-15			
; PRIOR APPLICATION NUMBER: GB 9805544.8			
; PRIOR FILING DATE: 1998-02-05			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: FastSeq For Windows Version 4.0			
; SEQ ID NO 7			
; LENGTH: 2262			
; TYPE: DNA			
; ORGANISM: Neisseria meningitidis strain M990			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)...(2259)			
US-10-735-098-7			
Query Match			
Best Local Similarity 57.7%; Score 1250.6; DB 17; Length 2262;			
Matches 1641; Conservative 0; Mismatches 429; Indels 63; Gaps 7;			
Qy	1	ATGTGTAAACCGAATATGCGGCAATGCTGTTGGTCCCTTACTTTGGCACTTCGATC	60
Db	1	ATGTGTAAACCGAATATGCGGCAATGCTGTTGGTCCCTTACTTTTAGCATCTTGATC	60
Qy	61	GGCGGCAATTCGGCGTGAGCTGTTGCGAATCAACCGCACCGC-----	108
Db	61	GGCGGCAATTCGGCGTGAGCTGTTGCGAATCAACCGCACCGC-----	108
Qy	109	TACCCCGTCACATTTTCAAGTCTAAGAGCTTCCCACTTCGCCCCCTCCGGGTCTTCGTA	168
Db	121	GATTCACATCTTCCATCTCTCGGATAAGCTGCTCCAGCTCCTCGCGAGCCTTCGTA	180
Qy	169	GAAACACGCGGTGCAACAGCGCGCGCTGCGTGGCGCAATGCGCTGTTGACACCGAAT	228
Db	181	GAAATCACGCGGTGCAAGCGCGCGCTGCGTGGCGCAATGCGGTGCGCAAGCGGAAT	240
Qy	229	ACTGCTTTTCATCGTAGAGTGGCAGCGCAATTCGCGATAGCAAAACAAGCAGAGAAAG	288
Db	241	ATCGCAACTTTTGATTAATATGTTATGTAATGTAATTTCCCAATAGTAAGCAGCAGAGGAT	300
Qy	289	CTGTCTGTTTAAAGAGGTGATGTTCTGTTTATACGGTTTCAAAAGAAATAACTTCAA	348
Db	301	CTGCCGTCTAAGAGAGGATATCTCTGTTTATAGCGGTACGCGGAAAGAACAGGCTGAC	360
Qy	349	CACCTTAAAGCGAAATTCATAACGTAATCCTGAGCAGCATTACCATCGGAAAT	408
Db	361	AAACTTTAAAGGAAATCAACGCGCGCATCTTAATGCAACCAATCTACACGTCGGATTA	420
Qy	409	GAAATATAAATAATATATTCGGTTTGTGTCAGTCCCGTTTGTGTTTACTATAAACA	468

Db	421	AAAGATCATCGTATCAATATAATAATATGTCGGGCGCGATATGTTTACTAGATATGGA	480
Qy	469	AAAGATCAAAATGAGAAAACATCGGATGAAAAGCAGTTTCTAATCTGTTAGGCTATGAC	528
Db	481	ACAGATGAAATCGAACAGAACTCAGCGGTAAAGCGGTTACCCACCGCTTAGGTTATGAC	540
Qy	529	GGTTTCTATATATCTCGGAGAACATCTTCCCAATCTTTTACCGAGCGGGAACGGTG	588
Db	541	GGTTTCTATATATCTCGGAGAACGCTCTTCCCAATCTTTTACCGAGTGGGGAACGGTG	600
Qy	589	AAATATTCGCGCAACTCGCAATATATGACCGATGCCATACGTCATCGGAGAGGTAAGGG	648
Db	601	GAATATTCGCTAATCGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTGAGCG	660
Qy	649	GTTTCCAGTGTGATTTGGTTTATACCATATATGTTGTAATGTAATTTGGGCGAGCTCT	708
Db	661	GTTGCGATTTGCAATTTGGGTTATATCATTTTATGTAACGATGTTGGTGCACTTCT	720
Qy	709	TATGAGCTAGGATGCGGATGCGCGGGAAGAAACATCTCGCAATATACGTTAATTTTC	768
Db	721	TATGCGCTAAGGATGTCGACGAAAGGAAAGCATCTCTGCAATATATACGTTGATTTT	780
Qy	769	GACAAAAAAACCTCGAAGGTAAGTTGATTTAAATCAGTATGTC---AAAAGAGAT	825
Db	781	GATAACAAAAACCATGATGCGAAGCTGATTTAAATCAGTATGTCGGAATAAAAAAGAT	840
Qy	826	GATCTTAAATTCACATGACCATTTTACCAACATTCACGCAACATTTGAGCGCAACCGCTT	885
Db	841	GAACCAAAAAACCGCTGACCATTTTACGACATTTCTGCAAAATTTGACGCGCAACCGCTT	900
Qy	886	ACCGGCTGCGCAAAAGTTAGCACCGAGGTGAAGACGCAACACGCTGTATGTAAGAAATTTG	945
Db	901	ACCGGCTGCGCAAGGTCAATCTGATTTAGCGAAAAACCTTGCGCGTAAATGAGCGTTG	960
Qy	946	TTTTTCCATACCGATGCGGCTTACAGTAAACGACACAGCTATTTCGGCGTGTTCGCGCAAA	1005
Db	961	TTTTTCCATGCGGATGCGGCTTACAGTAAACGACACAGCTATTTCGGCGTAAACGAGAA	1020
Qy	1006	GAGCTTGGCGGCGGTTTATCAGTAAACGACACAGCTATTTCGGCGTGTTCGCGCAAA	1065
Db	1021	GAGCTTGGCGGCGGTTTATCAGTAAACGACACAGCTATTTCGGCGTGTTCGCGCA--	1078
Qy	1066	CAAAAAACAGACACAGCAACCGCATCAGATACAAAATCTCGCCCTGCGCTCTGAAAAAC	1125
Db	1079	AAAAAACAGACACAGCAACCGCATCAGATACAAAACCTCGCCCTGCGCTCTGAAAAAC	1137
Qy	1126	ACCAAAATCTTGATTTCTTAAATTTCCGTTGAGGCGGCACTGATGACCATGCCGT	1185
Db	1138	ACCAAAATCTTGATTTCTTAAATTTCCGTTGAGGCGGCACTGATGACCATGCCGT	1197
Qy	1186	AGTTTGGCATTTCCATATGCGGATTTTGGTTCATCCGCAAAAATCTTGTGCAAGG	1245
Db	1198	AGTTTGGCATTTCTCTATGCGGATTTTGGTTCATCCGCAAAAATCTTGTGCAAGG	1257
Qy	1246	CGTGAATTTCTTGTGTTAGCCAAAGAAAACCATCGAGTTGCCGACGCGGAAAATG	1305
Db	1258	CGTGAATTTCTTGTGTTAGCCAAAGAAAACCATCGAGTTGCCGACGCGGAAAATG	1317
Qy	1306	ACCATCCGCTGTTGTTGCGATTTTCTGACTATGTAAGCTCGGACGCGGATAAAACCGAC	1365
Db	1318	ACCGTCCGCTGTTGTTGCGATTTTCTGACTATGTAAGCTCGGACGCGGATAAAACCGAT	1377
Qy	1366	CGCCCCCGCTCAAAACCGGAGGCGCAGGATGAAGAGGATTCGACATTTGATATGCGGAA	1425
Db	1378	CGCCCCCGCAATGTAACCAAGGCGGAGATGAAGGAGGATGAAGAGGATTCGAGGCGTT	1437
Qy	1426	GAAAGCGAAGCAAAATTTCCGGAAGATGATAACCGCGAGATGAAGTCAACGAGAGAG	1485
Db	1438	GATAACGACGAAGAAA---CGAAGACGAAGCGGTAGAACGAAAGCGCGGAGAGAC	1494
Qy	1486	GAAAGTGAAGAAACCGGAGGAGAACTGATGAAGACGAAGGAGGAGAACCGGAGAAACT	1545


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1495 GAAACT-----TCCGAAGAGGATAATGGCGAAGACGAAGAACCAACCGCCGGAAGAA 1548
1546 GAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA 1605
1549 ACCGAAGAGTTGATGAAGCCGAAGAGGAGGAGTTGAAGAACCCGAAGAACTGAAGAACTGAAG 1608
1606 ACAGAAAGAGGCAACCGCGGTTTCAGGACGATCCTCCGACATCCGACGAGGAGGAGGAGGAGG 1665
1609 ---CGAAGAGCAACCGCGGTTTCAGGACGATCCTCCGACATCCGACGAGGAGGAGGAGGAGG 1665
1666 AGGACATCGACTTTCTGAAAGGTATCCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1725
1666 AGGACATCGACTTTCTGAAAGGTATCCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1725
1726 GAAAGAGCAGCTATACCGGCTTTGGAAGGATCCGACGCGGAGGAGGAGGAGGAGGAGGAGGAG 1785
1726 GAAAGAGCAGCTATACCGGCTTTGGAAGGATCCGACGCGGAGGAGGAGGAGGAGGAGGAGGAG 1785
1786 GAAAGAGCAGCTATACCGGCTTTGGAAGGATCCGACGCGGAGGAGGAGGAGGAGGAGGAGGAG 1845
1786 AATCAGCGGATG-----AAAAAGCGGCAAAA 1812
1846 GCAGAAATGAGCTGATTTTGGTGGAGAGTCTTTCAGGTAGTTCAGGTAGTTCAGGTAGTTCAG 1905
1813 GCAGAAATTTACGTTGATTTTCAGCAAGAAATCGATTTCCGGAAGAGTTCAGGTAGTTCAGGT 1872
1906 GATACACACCGCGCTTTTATATTCGAAAGGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGG 1965
1873 GCGTAGAACCTGCTTTCCATATGAAGACGCGCAAGATTTGATGAGGAGGAGGAGGAGGAGGAG 1932
1966 TTGGCGCTACTCTGTAAGAAATGCTGATTTGCTGGGCAAGTTCGACTTAATCCCAAA 2025
1933 ACAGCGGCACTCGGAGGCGGATCAATCTTCGGAATGCTTCAGGAGGAGGAGGAGGAGGAGGAG 1992
2026 AGTTTAAAGCAGTAATCTTCTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2085
1993 ACATTCAGCTAGTAATCTTCTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2052
2086 TTGGGTGTAATATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2118
2053 TTGGCGGTACTATTTTCAATAATGATGGGAAA 2085

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RESULT 7

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US-10-343-561-15
; Sequence 15, Application US/10343561
; Publication No. US20040126389A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Dalemans, Wilfried
; APPLICANT: Denoel, Philippe
; APPLICANT: Dequesne, Guy
; APPLICANT: Feron, Christiane
; APPLICANT: Garcon, Nathalie
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Thiry, Georges
; APPLICANT: Thonnard, Joelle
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: Vaccines Comprising Outer Membrane
; TITLE OF INVENTION: Vesicles from Gram Negative Bacteria
; FILE REFERENCE: B45260
; CURRENT APPLICATION NUMBER: US/10/343.561
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/EP01/08857
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: EP 00956369.3
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: GB 0103170.7
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 15

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; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-561-15

Query Match      20.2%; Score 439.2; DB 17; Length 1000;
Best Local Similarity 71.4%; Pred. No. 1.7e-96;
Matches 681; Conservative 0; Mismatches 203; Indels 70; Gaps 5;

QY      1210 GATTTTGGTCATCCGACAAACTCTTCTGCGAAGGCGTGAATTCCTTTGGTAGCCAA 1269
Db      1 GATTTTGGTCATCCGACAAAGCTTCTTGTGCGAAGGCGTGAATTCCTTTGGTAGCCAA 60

QY      1270 GAGAAAACCATCGAGCTTCCGACGCGAGAAAATGACCATCCGTCGTTGTCGATTTT 1329
Db      61 GAGAAAACCATCAAGCTTCCCGATGGCAGGGAATGACCGTCCGTCGTTGTCGACATT 120

QY      1330 CTGACCTATGTAAACTCGGACGGATAAAAACCGACCGCCCGCCGTCGTAACCCGAGGCG 1389
Db      121 TTGACCTATGTAAACTCGGACGGATAAAAACCGACCGCCCGCAAGTAACCCAAAGCG 180

QY      1390 CAGGATGAAGAGGATTCGACATTTGATTAATGGCGAAGAAAGCAAGACGAAATTTCCGAA 1449
Db      181 GAGATATAAGGGA-----GGATGAAGAGAGTGCAGC 213

QY      1450 GATGATAACGCGAAGATGAAGTCAACCGAAGAAAGAGAGCTGAAGAAACCGAAGAGAA 1509
Db      214 GTTGTAACGTCGAAGAG-----GCCAAGGCGNAGTTTCCGAAGATGAAGCGGAGAA 267

QY      1510 ACTGATGAAGACGAAGAGGAGAAACCCGAGAAACTGAAGAAACTGAAGAAACTGAAGAA 1569
Db      268 GCCGAAGAAATCGTGAAGAAAGAAACCCGAGAAAGAGCTGAAGAGGAGAAAGCT---GAA 324

QY      1570 ACTGAAGAAACTGAAGAAACTGAAGAAACTGCGGACAGAGAGGAGGAGGAGGAGGAGG 1629
Db      325 CCCAAGAGTTGAAGAAACCGGAGAAATTCGCGACAGAAAGAGGAGGAGGAGGAGGAGG 384

QY      1630 GGCAGCATCTGCGCCACTCCGGAAGCCCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1689
Db      385 AACGCCATCTGCTGCTCGGAGGCTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 444

QY      1690 GGTATCGCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1749
Db      445 GGTATCGCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 504

QY      1750 TGGGAAGCGGTATCGGCGTCCGAGTAAGAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 1809
Db      505 TGGGAAGCGGTATCGGCGACACCCATTTCAATGGGAGCAATCAGGCGGAT-----552

QY      1810 ATCAAAAGGATAGCTATGCAATCAAGCGGCAAAAGCAGAAATTTGACGTTGATTTTGGT 1869
Db      553 -----AAAGAGCGGCAAAAGCAGAAATTTACCGTTAATTTCCGC 591

QY      1870 GCGAAGTCGCTTTCAGTAAGTTGACAGAAATAATGATACACACCCCGCTTTTATATT 1929
Db      592 GAGAAATCGAATTTCCGGAACGCTGACGAGAGAAACCGTGTACACACCTGCTTCTATATT 651

QY      1930 GAAAAAGGTGTGATGATGCGACGCTTCCGACGTTTGGCGGTACTCGTGAAGATGGT 1989
Db      652 GAAACGCGAAGATGAGGCGAACGCTTCCGACCAACAGCAGCAGCAGCAGCAGCAGCAGCAG 711

QY      1990 GTTGATTTGTCGGGCAAGGTTCCGACTAATCCCAAGTTTAAAGCCAGTAACTCTCTC 2049
Db      712 ATCAATCTTTCCGGAATGTTTCGACCAACCCAGAACCTTCCAGCTAGTAGTCTTCGT 771

QY      2050 GTAGAGGAGGATTTATGTCGCGAGGCGGAGAGTTCGGTGGTAAATATTATTCGACAGT 2109
Db      772 GTAGAGGAGGATTTTACGCGCCGCA--GCGAGGAAATTCGGCGGTATTATTTTCAATAAG 830

QY      2110 GACCGGAAATCGCGCTGTTATTCGGTTCGGAAGAAAGATATGAGGAGGAGGAGGAGGAG 2163
Db      831 GATGGGAAATCTCTTGGTAACTGAGGAGTACTGAAATAAAGTTGAAGTTGAA 884

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RESULT 8

US-10-087-192-463/c
; Sequence 463, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 31124
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (31124)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-463

Query Match 4.5%; Score 97; DB 13; Length 31124;
Best Local Similarity 64.4%; Pred. No. 3.3e-12;
Matches 145; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY	1391	AGGATGAAGAGATTTCGGACATTGATATGGCGAAGAACCGAAGCAAGAAATTCGGAG	1450
Db	18558	AAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	18499
QY	1451	ATGATAACGGCGAAGATGAAGTCACCGAAGAGAGAACTGAAGAAACCGAAGAA	1510
Db	18498	AAGAAGAGGAG	18439
QY	1511	CTGATGAACGACGAAGAGGAAGAACCCGAAGAACTGAAGAACTGAAGAACTGAAGAA	1570
Db	18438	AAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	18379
QY	1571	CTGAAGAACTGAAGAACTGAAGAAATCGCCGACAGAGAG	1615
Db	18378	AAGAAGAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGAGAG	18334

RESULT 9

US-10-027-632-269927/c
; Sequence 269927, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269927
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-269927

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Best Local Similarity 63.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 145; Conservative 1; Mismatches 84;

QY	1385	AGCGCAGGATGAAGAGATTTCGGACATTGATATGGCGAAGAACCGAAGCAAGAAATTT	1444
Db	452	AAG	393
QY	1445	CCGAAGATGATAACGGCGAAGATGAAGTCACCGAAGAGAGAGAGAGAGAGAGAGAGAG	1504
Db	392	GAGAAGGAG	333
QY	1505	AGAACTGATCAAGACGAG	1564
Db	332	AAG	273
QY	1565	AAGAACTGAAGAACTGAAGAACTGAAGAAATCGCCGACAGAGAA	1614
Db	272	AAGAAG	223

RESULT 10

US-10-027-632-269927/c
; Sequence 269927, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269927
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-269927

Query Match 4.4%; Score 95.2; DB 16; Length 635;
Best Local Similarity 63.0%; Pred. No. 1e-12;
Matches 145; Conservative 1; Mismatches 84; Indels 0; Gaps 0;

QY	1385	AGCGCAGGATGAAGAGATTTCGGACATTGATATGGCGAAGAACCGAAGCAAGAAATTT	1444
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QY	1445	CCGAAGATGATAACGGCGAAGATGAAGTCACCGAAGAGAGAGAGAGAGAGAGAGAG	1504

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-10-101-487-73

Query Match 4.2%; Score 91.4; DB 14; Length 530;
Best Local Similarity 61.6%; Pred. No. 8e-12; 91; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1379 AACCGAAGCGCAGGATGAAGAGGATTCGGACATTGATATGGCGAAGAAACCGGAGACG 1438
DB 523 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 464
QY 1439 AAATTTCCGAGATGATACCGCGGAAGATGAGTACCGAAGAGAGGAGGAGGAGGAGG 1498
DB 463 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 404
QY 1499 CCGAGAGGAAGAACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1558
DB 403 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 344
QY 1559 AAACCTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAG 1615
DB 343 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 287

RESULT 14
US-10-101-487-106
; Sequence 106, Application US/10101487
; Publication No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(537)
US-10-101-487-106

Query Match 4.2%; Score 91.4; DB 14; Length 554;
Best Local Similarity 61.6%; Pred. No. 8.2e-12;
Matches 146; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1379 AACCGAAGCGCAGGATGAAGAGGATTCGGACATTGATATGGCGAAGAAACCGGAGACG 1438
DB 20 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 79
QY 1439 AAATTTCCGAGATGATACCGCGGAAGATGAGTACCGAAGAGAGGAGGAGGAGGAGG 1498
DB 80 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 139
QY 1499 CCGAAGAGAACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1558
DB 140 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 199

QY 1559 AAACCTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAG 1615
DB 200 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 256

RESULT 15
US-09-864-761-2534/c
; Sequence 2534, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2534
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011416.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 35
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_phi.*

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12: gb_sy.*

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14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_fod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2226	100.0	2226	1	AF123380	AF123380 Neisseria
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3	2226	100.0	2226	6	BD074757	BD074757 Neisseria
4	1774.8	79.7	326301	1	NMA622491	AL162757 Neisseria
5	1538.6	69.1	2519	1	AF072890	AF072890 Neisseria
6	1499.8	67.4	2124	1	AF123383	AF123383 Neisseria
7	1499.8	67.4	2124	6	A98976	A98976 Sequence 9
8	1499.8	67.4	2124	6	BD074759	BD074759 Neisseria
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13	1487	66.8	2537	1	AF031432	AF031432 Neisseria
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15	1477.2	66.4	349980	6	AX044033	AX044033 Sequence
16	1442.2	64.8	2262	1	AF123381	AF123381 Neisseria
17	1442.2	64.8	2262	6	A98974	A98974 Sequence 7
18	1442.2	64.8	2262	6	BD074758	BD074758 Neisseria
19	1375.8	61.8	2169	1	AF123382	AF123382 Neisseria
20	1375.8	61.8	2169	6	A98970	A98970 Sequence 3
21	1375.8	61.8	2169	6	BD074756	BD074756 Neisseria
22	716	32.2	1000	6	AX081510	AX081510 Sequence
23	716	32.2	1000	6	AX374691	AX374691 Sequence
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25	239.8	10.8	3300	1	NGU16260	U16260 Neisseria g
26	239.8	10.8	3300	6	AX685922	AX685922 Sequence
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33	97.6	4.4	263081	2	AC115498	AC115498 Rattus no
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35	97	4.4	219626	10	AC098719	AC098719 Mus muscu
36	96.2	4.3	189483	2	AC120267	AC120267 Rattus no
37	96.2	4.3	205161	2	AC115451	AC115451 Rattus no
38	96.2	4.3	210322	2	AC123582	AC123582 Rattus no
39	96.2	4.3	247106	2	AC108255	AC108255 Rattus no
40	96.2	4.3	260973	2	AC119104	AC119104 Rattus no
41	96.2	4.3	269126	2	AC106218	AC106218 Rattus no
42	96	4.3	213609	10	AC127341	AC127341 Mus muscu
43	95.8	4.3	179685	10	AC122056	AC122056 Mus muscu
44	95.6	4.3	94333	2	AC140495	AC140495 Rattus no
45	95.6	4.3	214976	2	AC114151	AC114151 Rattus no

ALIGNMENTS

RESULT 1	AF123380	2226 bp	DNA	linear	BCT 24-MAY-1999
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DEFINITION	AF123380.1	GI:4884686			
ACCESSION	Neisseria meningitidis				
VERSION	Neisseria meningitidis				
KEYWORDS	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
SOURCE	Neisseriaceae; Neisseria.				
ORGANISM	1 (bases 1 to 2226)				
REFERENCE	Patterson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and				
AUTHORS	Tomassen,J.				

Pred. No. is the number of results predicted by chance to have a

Thu Aug 26 10:18:15 2004

us-10-735-098-5.rge

Sequence variability of the meningococcal lactoferrin-binding

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 2226)
Petersson, A., van der Biezen, J., Joosten, V., Heydriksen, J. and Tomassen, J.
Direct Submission
Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
Location/Qualifiers
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K"

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 2226)
Petersson, A., van der Biezen, J., Joosten, V., Heydriksen, J. and Tomassen, J.
Direct Submission
Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
Location/Qualifiers
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/organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/strain="H44/76"
/db_xref="taxon:487"
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/db_xref="GI:4884687"
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source

gene

CDS

ORIGIN

Query Match 100.0%; Score 2226; DB 1; Length 2226;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION A98972.1 GI:6781932
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ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Petersson-Fernholm, A.M. and Tommassen, J.P.
TITLE NEISSERIA LAQTOFERRIN BINDING PROTEIN
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UNIV UTRICHT (NL); PETERSSON FERNHOLM ANNIKA MAR (NL)
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 0;
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Query Match      69.1%; Score 1538.6; DB 1; Length 2519;
Best Local Similarity 83.7%; Pred. No. 2.3e-302;
Matches 1865; Conservative 0; Mismatches 319; Indels 45; Gaps 9;

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RESULT 6
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LOCUS
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Neisseria meningitidis strain 881607 lactoferrin-binding protein precursor (lbpB) gene, complete cds.
ACCESSION
AF123383
VERSION
AF123383.1 GI:4884692
KEYWORDS
SOURCE
ORGANISM

Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tomassen,J.

Sequence variability of the meningococcal lactoferrin-binding protein lbpB
Gene 231 (1-2), 105-110 (1999)
10231574
PUBMED
2 (bases 1 to 2124)
Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tomassen,J.

Direct Submission
Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
Location/Qualifiers

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FEATURES
source

gene

CDS

ORIGIN

Query Match 67.4%; Score 1499.8; DB 1; Length 2124;
Best Local Similarity 83.3%; Pred. No. 1.7e-294;
Matches 1779; Conservative 0; Mismatches 317; Indels 39; Gaps 5;

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BD074759
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

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 Neisseria lactoferrin-binding protein.

BD074759
 GI:22620362

JP 2001514894-A/5.

unidentified

unclassified.

unclassified.

1 (bases 1 to 2124)

Fellholm, A.M.P. and Thomsen, J.P.M.

Neisseria lactoferrin-binding protein

Patent: JP 2001514894-A 5 18-SEP-2001.

UNIVERSITY OF UTRICHT, TECHNOLOGY FOUNDATION

OS Unidentified

PN JP 2001514894-A/5

PD 18-SEP-2001

PF 10-AUG-1998 JP 2000509840

PR 15-AUG-1997 GB 9717423.9, 05-FEB-1998 GB 9802544.8 PI

ANICA MARGARETA PETERSON FELNHOLM, JOHANES PETRUS MARIA PI

THOMASEN

PC C12N15/09,A61K39/095,A61K39/395,A61K48/00,A61P31/12,C07K14/22,
PC C07K16/12,
PC C12N1/21,C12P21/02,C12P21/08,G01N33/15,G01N33/50,G01N33/68, PC
C12N15/00

CC Strandedness: Double;
CC Topology: Linear;
CC Neisseria lactoferrin-binding protein
FH Key Location/Qualifiers
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/organism='Unidentified'.
FT Location/Qualifiers
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Matches 1779; Conservative 0; Mismatches 317; Indels 39; Gaps 5;

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VERSION A98968.1 GI:6781928
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Neisseria meningitidis
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 2277)
Petersson-Fernholm, A.M. and Tommassen, J.P.
NEISSERIA LACTOPERRIN BINDING PROTEIN
Patent: WO 9909176-A 1 25-FEB-1999;
UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIKA MAR (NL)
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 KEYWORDS JP 2001514894-A/1.
 SOURCE unidentifed
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 2277)
 AUTHORS Felnholm,A.M.P. and Thomasen,J.P.M.
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 JOURNAL Patent: JP 2001514894-A 1 18-SEP-2001;
 UNIVERSITY OF UTRICHT,TECHNOLOGY FOUNDATION
 COMMENT OS Unidentified
 PN JP 2001514894-A/1
 PD 18-SEP-2001
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Query Match 66.9%; Score 1490.2; DB 6; Length 2277;
 Best Local Similarity 82.7%; Pred. No. 1.6e-292;
 Matches 1859; Conservative 0; Mismatches 298; Indels 90; Gaps 10;
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 QY 1258 ATTTCTCTATGCGCGGATTTGGCTCATCCGCAAACTCTTGTGCGAAGGCGATGAAT 1317
 Db |||||
 QY 1261 CTTTGGTTAGCCAAAGAGAAAAACCATCGAGCTTCCGACGCGGAGGAAATGACCGTCCGT 1320
 Db |||||
 QY 1318 CTTTGGTTAGCCAAAGAGAAAAACCATCGAGCTTCCGACGCGGAGGAAATGACCGTCCGT 1377
 Db |||||
 QY 1321 GCTTGTGCGATTTCTGACTATGTGAAACTCGGACGAGTAAATAATGACCGCGGCA 1380
 Db |||||
 QY 1378 GCTTGTGCGACTTTTGAACCTCGGACGAGTAAATAATGACCGCGGCA 1437
 Db |||||
 QY 1381 AGTAAACCAAGCGGAGATAAAGGAGAGATGAAGAGATCAGCGTTGTTGTAACGAC 1440
 Db |||||
 QY 1438 GCCAAACCGAAGG---GCAGGACGAGAGATTCGGACATATGATATGTC 1485
 Db |||||
 QY 1441 GAAGAAGCGCAAGAGATGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
 Db |||||
 QY 1486 GAAGAAGC---GAAGACGAAATTCGGCGATGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1542
 Db |||||
 QY 1501 GATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560

Db	1543	GGATGAAGCGACGGAAGAGACGAGCCACAGAAACGAGCGGAGAGACGAA	1602
Qy	1561	GCTCAAGAACCTGAAGAACCCGAGAGAAATCGCCGAGAGCGCGTGGTGTCA	1620
Db	1603	GCTGAGAGACT-----GAGAGAGATCGTCGGCAGAGGCAAC---GGCAGTTCA	1650
Qy	1621	GACGCAATCTGCGCGCTCCGAGAGCTCTAAAGCAGGAGATTCGACCTTTCTTGAA	1680
Db	1651	AACGCCATCTGCTGCTCCGAGAGCTCTAAAGCAGGAGATTCGACCTTTCTTGAA	1710
Qy	1681	GATATCCGACGCGGAGAGCGACATTCGCAAACTGGAAGACGCTATACCGGCACT	1740
Db	1711	GATATCCGACGCGGAGAGCGATTCGCAAACTGGAAGACGCTATACCGGCACT	1770
Qy	1741	TGGGAAGCGCGTATCAGCAAAACCCATTCATATGGAACATATCGGATATAAAGCGCA	1800
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Qy	1801	AAAGCAGAAATTCAGCTGATTCGCGAGAAATCGATTCGGAACGCTGACGAGAA	1860
Db	1831	AAAGCAGAAATTCAGCTGATTCGCGAGAAATCGATTCGGAACGCTGACGAGAA	1890
Qy	1861	AACGCTGACAACTGCTTTTCATATGAAACGCGGATGATGAGGCAATGTTTCCAC	1920
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Qy	1921	GGCAGACGCGCACTCGGATACGCGATCAATCTTTGGGAAATGATTCGATCT	1980
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Qy	1981	CCAAGTTTCAAGCGCAATATCTTCTGTAACAGCGGCTTTACGCGCGCAGCGAG	2040
Db	2011	CAGATCTTCAAGCGCAATATCTTCTGTAACAGCGGCTTTACGCGCGCAGCGAG	2070
Qy	2041	GAATGGCGGCTATTTTCAATATGATGGAATCTCTTGGTATACTGAAGATCT	2100
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Qy	2142	--TGGCGACAGTTAAACCTGAAGCTAAACCCCAATTCGGCTGCTATTTCGTCGCAAG	2199
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Qy	2200	AAAGATAATAAGAGAGCTGGAATAATCA	2226
Db	2251	AAAGATAATAAGAGAGCTGGAATAATCA	2277
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LOCUS			BCT 11-JUN-2001
DEFINITION	Neisseria meningitidis lactoferrin binding protein B precursor (lbpB) and lactoferrin binding protein A precursor (lbpA) genes, complete cds.		
ACCESSION	AF049349		
VERSION	AF049349.1	GI:3582727	
KEYWORDS	Neisseria meningitidis		
SOURCE	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
ORGANISM	1 (bases 1 to 5691)		
REFERENCE	Lewis, L.A., Rohde, K., Gipson, M., Behrens, B., Gray, E., Toth, S.I., Roe, B.A., and Dyer, D.W.		
AUTHORS	Identification and molecular analysis of lbpB, which encodes the two-component meningococcal lactoferrin receptor		
TITLE	Infect. Immun. 66 (6), 3017-3023 (1998)		
JOURNAL	9596785		
MEDLINE			
PUBMED			

REFERENCE	2 (bases 1 to 5691)
AUTHORS	Lewis, L.A., Rohde, K., Gipson, M., Behrens, B., Gray, E., Toth, S.I., Roe, B.A., and Dyer, D.W.
TITLE	Direct Submission
JOURNAL	Submitted (19-FEB-1998) Microbiology and Immunology, University of Oklahoma Health Sciences Center, 1035 EMSB / 940 SL Young Blvd., Oklahoma City, OK 73014, USA
FEATURES	Location/Qualifiers
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	/db_xref="taxon:487"
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repeat_region	176..432
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gene	527..2770
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misc_signal	550..568
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	/evidence="experimental"
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CDS	593..2770
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RKSGYSDMDRFDGLYFVPLNEWKGDQLIRGLKYSRTKFIDEHRRRRMGLLY		Qy	961	CATACCGATGCGGATCAGCGGCTTCAGGGCGGTTTTTTCGGCGATAAGGGGGAAGAGCTT	1020
RYENKYSNNWADKAVLSDFKQVATDNNLKLNCAPVAVDKSRASCRASDPYSDSS		Db	1538	CATGCGGATGCGGATCAGCGGCTTCAGGGCGGTTTTTTCGGCGATAAGGGGGAAGAGCTT	1597
DFPHREHNVNLAASFELSKNKTWHHTLTLFGYDASNAISRPEKSHNAARISEYS		Qy	1021	GCCGAGCGGTTTATCAGCAACGACAAACAGCGTATTCGCGGATTCGCGAGGCAAAAAACA	1080
DTYDGKYLKLGKPEVGVSCYIETLASREKVPKRNHFSLSVRSRSGPTPSFOE		Db	1598	GCGGAGCGGTTTATCAGCAACGACAAACAGCGTATTCGCGGATTCGCGAGGCAAAAAACA	1653
FSSGGRYDKRNTTSEELVRSYVDRSWSGIVKPNRHSLSVRSRSGPTPSFOE		Qy	1081	AACGATCAACGACGACAGATACAAATCTGCTATGCTGCTGTAAGGCAACCAAAATC	1140
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Best Local Similarity 82.7%; Pred. No. 1.7e-292;		Qy	1441	GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1500
Matches 1859; Conservative 0; Mismatches 298; Indels 90; Gaps 10;		Db	1979	GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2035
Qy 1 ATGTGTAACCGAATTATGGCGGCAATGCTTGTGTTGCCCTTACTTTTGGCACTTGTATT		Qy	1501	GATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1560
Db 593 ATGTGTAACCGAATTATGGCGGCAATGCTTGTGTTGCCCTTACTTTTGGCACTTGTATT		Db	2036	GGAGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2095
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Qy 121 TTCAAGTCTAAGAGCTTCCACCTCCGCTCCGCAACCTTCTATAGAAATCAACGCG		Qy	1621	GACGGATCTTCCGCGTCCGAGGCTCTTAAAGGAGGAGGATTCGACCTTTTCTGAA	1680
Db 713 TTCAAGTCTAAGAGCTTCCACCTCCGCTCCGCAACCTTCTATAGAAATCAACGCG		Db	2144	AACGCCATCTCTGCTGCTCCGGAAGCTCTTAAAGGAGGAGGATTCGACCTTTTCTG	2203
Qy 181 GTGCGGTCACCGGCGCTCGGTCGCGCAATGCGGCTGTTGAGCGGATTTTCGCA					
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Db	2264	TGGGAAGCGCGTATCGGCAAAACCCATTCATGGGACAAATCATCGGATATAAGAGCGGCA	2323
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Db	2384	AACGCTGTAGAACCTGCTTTCCGTATTGAAACCGCGGTATGAGGCAACGGTTTCCAT	2443
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Db	2744	AAAGATAATAAGAGGTGAAAAATGA	2770
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LOCUS			
DEFINITION			
Neisseria meningitidis B16B6 lactoferrin binding protein B			
precursor (lbpB) gene, complete cds.			
ACCESSION			
AF031432			
VERSION			
AF031432.1			
KEYWORDS			
SOURCE			
ORGANISM			
Neisseria meningitidis			
Neisseria meningitidis			
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
Neisseriaceae; Neisseria.			
REFERENCE			
1 (bases 1 to 2537)			
Bonnah, R.A. and Schryvers, A.B.			
Preparation and characterization of Neisseria meningitidis mutants			
deficient in production of the human lactoferrin-binding proteins			
LbpA and LbpB			
J. Bacteriol. 180 (12), 3080-3090 (1998)			
JOURNAL			
MEDLINE			
PUBMED			
98292739			
REFERENCE			
2 (bases 1 to 2537)			
Bonnah, R.A. and Schryvers, A.B.			
Direct Submission			
Submitted (24-OCT-1997) Microbiology & Infectious Diseases,			
University of Calgary, 3330-Hospital Drive N.W., Calgary, AB T2N			
4N1, Canada			
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Query Match			
Best Local Similarity			
Matches 1857; Conservative			
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QY	61	GGCGGCAATTTCCGGGTGCGAGCTGTTGTCGAATCAACCGCACCGCTACCCCGTCACT	120
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QY	121	TTCAAGTCTAAGAGCGTTCCCACTCCGCCCTCCCAACCTTCTATAGAAACACGCGG	180
Db	480	TTCAAGTCTAAGAGCGTTCCCACTCCGCCCTCCCAACCTTCTATAGAAACACGCGG	539
QY	181	GTGCCGTCAACCGGCGCTCCGTCGTCGGCAATCGGGTGTGTAGAGCGGATTTTCGCA	240
Db	540	GT-----CAACCGGCGCGCTCCGTCGTCGGCAATCGGGTGTGTAGAGCGGATTTTCGCT	593
QY	241	ACTTCTGATAAGGTTGCGCAATGATTTTCCAAATAGCAAAACAGCAGAGAAAGCTGTGC	300
Db	594	TTTCATCTGTAAGATGCGCGAATTCGAATAGCAACAGCAGAGAAAGCTGTGC	653
QY	301	TTTAAAGAGGTCATGTTCTGTTTTTATACGGTTCAAAAAGATAACTTCAGTGGCTT	360
Db	654	TTTCAAGAGGTCATGTTCTGTTTTTATACGGTTCAAAAAGATAACTTCACAACTT	713
QY	361	AGGATAAAATTCATCAACGCAATCTTAATGTAGAAATAGGACATCAGAAATGAAAT	420

Db	714	AAAAAGCGAAATTCATAAAGCTGATTCGCGATGTAGAAATTAGGACATCAAGAAAGCGAAAT	773
Qy	421	AAAAAATATGGTTATGAAATTTCTGGATCGCGGTTATGTATATATCTAAAAACGGACAGAT	480
Db	774	AAAAAATATGATTATAAATTTGTAGATCGAGGTTATGTATA---TGTTAAAGGGAAGAAT	830
Qy	481	GAAATTTAGTGACATTCAAATCGCAAGCAGTTTCTAATCGTTTGTGGCTACGACGGTTTT	540
Db	831	GAAATTAAGTGGACTTCAGATTACAAGCAGTTTCCAAACCGCTTAGGTTATGACGCGTTTT	890
Qy	541	GTATATATTTCGGAGAAACCTCTCCCAATCTTTACGAGCGGGGAAACGGTCAATAT	600
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Qy	601	TCCGTTAACTGSCAATATATGACCGATGCCATAGCTCATCGAACAGGAAAGCAGGAGAT	660
Db	951	TTTGTGTAACCTGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTAAAGC---GGTT	1007
Qy	661	CCTAGCGAAGATTTGGGTTATCTCGTTTATTACGGTCAAAATGTCGAGCAACTTCTTAT	720
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VERSION
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KEYWORDS
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AUTHORS
 Tetzelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
 Dodson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
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 Rappuoli, R. and Venter, J.C.

Complete genome sequence of Neisseria meningitidis serogroup B strain MC58

Science 287 (5459), 1809-1815 (2000)

JOURNAL MEDLINE

PUBMED 20175755

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Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
 Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
 Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
 Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
 Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,
 Cittone, H., Clark, E.B., Cotton, M.D., Utterback, I.R., Khouri, H.,
 Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Masignani, V.,
 Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
 Rappuoli, R. and Venter, J.C.

Direct Submission

Submitted (17-MAR-2000) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

Location/Qualifiers

FEATURES

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LOCUS

DEFINITION

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ACCESSION

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VERSION

AX044033.1 GI:11342917

KEYWORDS

Neisseria meningitidis

SOURCE

Neisseria meningitidis

ORGANISM

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

REFERENCE

1

AUTHORS

Pizza, M.; Hickey, E.; Peterson, J.; Tettelin, H.; Venter, J. C.; Masignani, V.; Galeotti, C.; Mora, M.; Ratti, G.; Scarfelli, N.; Scariato, V.; Rappuoli, R.; Frazer, C. M. and Grandi, G.

TITLE

Neisseria genomic sequences and methods of their use

JOURNAL

Patent: WO 0066791-A 112 09-NOV-2000;

CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)

FEATURES

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Query Match 66.4%; Score 1477.2; DB 6; Length 349980;

Best Local Similarity 81.4%; Pred. No. 9.7e-290;

Matches 1832; Conservative 0; Mismatches 358; Indels 60; Gaps 8;

Qy 1 ATGTGTAAACCGAATATGCGGCATGTCCTGTTGCGCCCTACTTTGSCATCTTGTTAT 60

Db 99481 ATGTGTAAACCGAATATGCGGCATGTCCTGTTGCGCCCTACTTTAGCATCTTGATC 99422

Qy 61 GCGGCAATTTGCGCGTGCAGCTGTTGTGCAATCAACGCCGACCGCGTACCCCGTCACT 120

Db 99421 GCGGCAATTTGCGCGTGCAGCTGTTGTGAAATCAACGCCGACCGCGTACCCCGTCAAC 99362

Qy 121 TTCAAGTCTAAGAGCGTTCCTCACTCCCGCCCTGCGCAAACTTCTATAGAAACACCGCG 180

Db 99361 TTCAATCTAAGGAGCTTCCCACTCCCGCCCTGCGGGTCTTCGGTAGAAACACCGCG 99302

Qy 181 GTGCGGTCAACCGGCTGCGGTGCGGCAATGCGGCTGTTGAGCGGATTTTCGCA 240

Db 99301 GT-----CAACCGCCCGCGTGGCGCAATGCGGCTGCCAAGGGAATATTGCT 99248

Qy 241 ACTTCTGATAGGTGGCAATGATTTTCCAAATAGCAAAACAGCAGAGAAAAGCTGTCG 300

Db 99247 TCCTATAACAAGAGCTGACGGAATTTCCGCAAGCATCAGGCAGAGGAGCATCTGCG 99188

Qy 301 TTTAAAGAGGTGATGTTCTGTTTTATACGGTTCAAAAAGATAAATCTTCACTGCGCT 360

Db 99187 CTTAAAGAGAGGATATCTCTGTTTTAGACGGTACGCTGAAAGAACAGGCTGACAACT 99128

Qy 361 AAGGATAAAAATTCATCAACGCAATCTTAATGTAGAAATTAGGACATCAGAAAAATCAAA 420

Db 99127 AAAAAGAAATCAACGAAAGCTATTCATGCTGAGGGTTATCACATCGAAAAAAGAGAA 99068

Qy 421 AAAAATATGTTATGAAATTTGTGATGCGCGGTATGATATATCTAAACCGRAACA --- 477

Db 99067 GAAAAATATCAATATCAATTTGTCGCGGCTATGTTTACAGGCGGGAAGAAAG 99008

Qy 478 ---GATGAAATTTGAGTGAGCTTCAATCGCAAGCAGTTTCTTAATCTGTTGGCTACGAC 534

Db 99007 GATTAATGAAAAAAGAAAGACTTCTGATGTTGAAGGTTTGTAAACCGATTTAGTTATGAC 98948

Qy 535 GGTTTGTATATTTATTCGGAGAAATCTTTCCCAATCTTTTACCAGCGCGGAAACGGTG 594

Db 98947 GGTTTGTATATTTATTCGGAGAACTTCTTCCCAATCTTTTACCAGCGCGGAAACGGTG 98888

Qy 595 CAATATTCGGTAACTGCGCAATATATGACCGATGCGCATGCTCATCGAACAGGAAAAAGCA 654

Db 98887 CAATATTCGGTAACTGCGCAATATATGACCGATGCGCAATGCTCATCGAACAGGTAAGG- 98829

Qy 655 GGAGATCTTAGGAAGATTTGGTTATCTCTGTTTATACGTTTCAAAATGTGCGACCACT 714

Db 98828 --GGTTCCAGTACGATTTGGTTATACCAATATTTATGTAATGAAATTTGGGCACT 98771

Qy 715 TCTTATGCTGCGACTGCGCGACGACCGGAGGAGAAACATCTCTCCGCAATATACGTTGAT 774

Db 98770 TCTTATGAGCTAGGATGCGCGACGACGAGGAAAGCATCTCTCCGCAATATACGTTGAT 98711

Qy 775 TTGATAAGAAAACTTTGACGGGTCAATTAATTAATAATCAGTATGTGCAAAAGAAAAACC 834

Db 98710 TTTGATAACAAAAACCTGATGCGCAAGCTGATTTAAAAATCAGTATGTGCAAAATAAAA 98651

Qy 835 GATGAA-----AAGAAACCACTGACCATTTACGACATTTACCGCAACATTTGACCGC 885

Db 98650 AATCCAAATGAGCCCAAAAAACCGCTGACCATTTACGACATTTACCGCAACATTTGACCGC 98591

Qy 886 AACCGCTTTACCGCAGTGCCTAAAGTTAAACACCGAGTTGAAGACGAGCCACGCTGATAA 945

Db 98590 AACCGCTTTACCGCAGTGCCTAAAGTTAGCACCGAGGTGAAGACGCAACAGCTGATAA 98531

Qy 946 GAGCATTTGTTTTCCATACCGATGCGGCTGATGCGGCTTTGAGGCGGTTTTTTCGGCAT 1005

Db 98530 GAATATTTGTTTTCCATACCGATGCGGCTGATGCGGCTTTGAGGCGGTTTTTTCGGCAT 98471

Qy 1006 AAGGGGAGAGCTTTGCGCGAGCTTTATCAGCAACACACAGCGTATTGCGCGTATTTC 1065

Db 98470 AACGGAAGAGCTTTGCGCGAGCTTTATCAGCAACACACAGCGTATTGCGCGTATTTC 98411

Qy 1066 GCAGGCA---AAAAACAAACCGCATCAACACGAGCAGATACAAATCTTCTGATCGGCT 1122

Db 98410 GCAGGCAACAAACAAACAGAGACAGAAAAACGAGCAGATACAAAACTGCCCTGCTCT 98351

Qy 1123 GAAAAACACCAAAATCTTGGATTTCTGAAAAATTTCCGTTGACGAGCGGAGGATAA 1182

Db 98350 GGAAAAACACACCAAAATCTTGGATTCTCTGAAAAATTTCCGTTGACGAGCAAGTGATAAA 98291

QY 1183 AATGCCCGCGGTTTCCCAATTTCCCTCTGCCGATTTTGGCCATCCCGACAACTTCCTT 1242

Db 98290 AATCCCGTGAGTTTCCCAATTTCCCTCTATGCCGATTTTGGTTCATCCGACAACTTCCTT 98231

QY 1243 GTCGAAGGCGGTGAATTCCTTTGGTTAGCAAGAGAAACCAATCGAGCTTCGCGACGCG 1302

Db 98230 GTCGAAGGCGGTGAATTCCTTTGGTTAAACAAGAACAAACCATCGAGCTTCGCGATGT 98171

QY 1303 AGGAAATGACCGTTCGCTGCTTGGTTGCGATTTTCTGACCTATGTGAAACTCGGACGGATA 1362

Db 98170 AGGAAACGACAATCCGAACCTCTGCGATTTTCTGACCTATGTGAAATCGGACGGATG 98111

QY 1363 AAAACTGACCGCCCGACAGTAAGTAAACCAAGGCGGAAGTAAAGGGAAGGATGAAGAGAT 1422

Db 98110 CAAACCGAACGTTCCCGCCGCAAAACCGAAGGCGGAGGAGAAAGAGGAGGACCAAGAGGAT 98051

QY 1423 ACAGCGTTGTGTAAACGAGCAAGAGCGACGGAAGATGAAGCCGACAGAGGCGAGCGAAGGA 1482

Db 98050 ACAGCGTTGTATAGCGTTCGAAGAGCGGAAGACGAAATCGACGATGAA -----GAAGGC 97997

QY 1483 GGCGAAGACGGAATCGGCGATGAAGGAGAGGTGCGGAAGACGAAGCCGCAAGAAACGAA 1542

Db 97996 ACCGAAGACGCGCGGTAAAGACGAAGCGACGGAAGACGAAGCGGTAGAAGGTGAA 97937

QY 1543 GGCGGCGAAGAGACGAGCTGAAGAACCTGAAGAACCGGAGAGAGATCGCCGCGAGAA 1602

Db 97936 -----GATGAAGCTGAAGAACCCGGAAGAGAAATCGCCGACAGAA 97898

QY 1603 GGCGGCGGTGTGTTCAGCGGATCTCTGCCGCTCCGGAAGCTCTCTAAAGGCGAGGAT 1662

Db 97897 GAAGCGGCGCGGTTTCAGACGGCATCTGCCGCTCCGGAAGCCCTTAAAGGCGAGAAC 97838

QY 1663 ATCGACCTTTTCTTGAAAGGTATCGGACGCGGGAAGCGGACATTCGCGCAAACTGGAATA 1722

Db 97837 ATCGACCTTTTCTTGAAAGGTATCGGACGCGGGAAGCGGATTCGGAACCTGGAGAA 97778

QY 1723 GCAGCTATACCGGCACCTTGGGAAGCGGTATCAGCAACCCATTCATGGGACAAATCAT 1782

Db 97777 GCACACTATACCGGCACCTTGGGAAGCGGTATCGGCAACCCATTCATGGGACAAATCAG 97718

QY 1783 CGGNTAAAGCGGCAAGAGAAATTTGACGTTGATTTCCGCGAGAAATCGATTTCC 1842

Db 97717 CGGNTAAAGCGGCAAGAGAGATTTACCGTTGATTTCCGCAAGAAATCGATTTCC 97658

QY 1843 GGAACGCTGACGGAGAAACGGTGTACACCTGCTTTCCATATTTGAAACGCGCGTCAAT 1902

Db 97657 GGAACGCTGACGGAGAAACGGTGTAGAACCTGCTTTCCATATTTGAAACGCGCAAGATT 97598

QY 1903 GAGGGCAATGGTTTCCACGCGACAGCGCGCACCTCGGATTAACGGCATCAATCTTTGCGGA 1962

Db 97597 GAGGGCAACGGTTTCTACGCGACAGCACGCGCATCGGGAACCGGCATCAATCTTTGCGGA 97538

QY 1963 ATGATTTCGACTAATCTCTCAAGTTTCAAAGCCAAATCTTCTTGTAAACGCGGCTTT 2022

Db 97537 AATGGTTTCGACCGACCCCAAACTTCCAAGCTAGTAATCTTCTGTAGAGGGGGATTT 97478

QY 2023 TACGGCCCGCAGCGGAGGAAATTTGGCGGTACTATTTTCAATAATGATGGGAAATCTCTT 2082

Db 97477 TACGGCCCGCAGCGGAGGAAATTTGGCGGTATTTATTTTCAATAATGATGGGAAATCTCTT 97418

QY 2083 GGTATAACTGAAGATACTGAAAA-----TGAAGCTGAAGCTGAAGTTGAAATGAAGCT 2136

Db 97417 GGTATAACTGAAGTACTGAAAATAAAGTTGATGTTGAAGCTGAAGTTGATGCTGAAGTT 97358

QY 2137 GGTGTTGGCAACAGTTTAAACCTGAAGCTTAAACCCCAATTCGCGGTGTTATTCGTCGCG 2196

Db 97357 GATGTTGGCAACAGTTTAGAATCTGAAGTTAAACCAATTCGCGGTGTTATTCGTCGTCG 97298

QY 2197 AAGAAAGATAATGAAGAGTGGAAAAATGA 2226

Db 97297 AAGAAAGATATGCAGGAGGTGAAAAATGA 97268

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:48:44 ; Search time 754.168 Seconds
(without alignments)
12538.967 Million cell updates/sec

Title: US-10-735-098-5
Perfect score: 2226
Sequence: 1 atgtgtaaacgaattatgg.....ataaagaggtggaataatga 2226

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2226	100.0	2226	2	AAX23321	Aax23321 N. mening
2	1774.8	79.7	2226	7	ACA41945	Aca41945 Prokaryot
3	1499.8	67.4	2124	2	AAX23323	Aax23323 N. mening
4	1490.2	66.9	2277	2	AAX23319	Aax23319 N. mening
C 5	1477.2	66.4	110000	3	AA481489_1	Continuation (2 of
C 6	1477.2	66.4	349980	3	AA481489_1	Continuation (2 of
7	1442.2	64.8	2262	2	AAX21611	Aaf21611 Neisseria
8	1375.8	61.8	2169	2	AAX23322	Aax23322 N. mening
C 9	1077.6	48.4	14652	3	AAA81482	Aax23320 N. mening
10	716	32.2	1000	4	AAAF91389	Aaf91389 N. mening
11	716	32.2	1000	6	ABK37769	Abk37769 DNA seque
12	390.4	17.5	707	3	AAA81815	Aaa81815 N. mening
13	239.8	10.8	3300	6	ABK67377	Abk67377 Neisseria
14	91.2	4.1	379	5	AAAS90909	Aas90909 DNA encod
15	91.2	4.1	379	5	AAAS75428	Aas75428 DNA encod
16	91.2	4.1	379	9	ADRO9716	Ade09716 Novel DNA
17	90.2	4.1	621	5	AAAS90688	Aas90688 DNA encod
18	89.8	4.0	400	5	AAAS75460	Aas75460 DNA encod
19	89.8	4.0	963	5	AAAS68580	Aas68580 DNA encod
C 20	87	3.9	453	5	AAAS92079	Aas92079 DNA encod
21	87	3.9	1072	5	AAAS90738	Aas90738 DNA encod
22	87	3.9	49999	2	AAZ23896	Aaz23896 Murine LO
23	87	3.9	49999	2	AAZ23891	Aaz23891 Murine LO

24	86.6	3.9	801	5	AAS90729	Aas90729 DNA encod
25	85.4	3.8	3399	2	AAT05868	Aat05868 Chicken 1
26	84.6	3.8	708	5	AAS69547	Aas69547 DNA encod
27	84.6	3.8	708	5	AAS75461	Aas75461 DNA encod
28	83.8	3.8	441	5	AAS75453	Aas75453 DNA encod
29	83.8	3.8	1684	5	AAS90724	Aas90724 DNA encod
30	83.8	3.8	29392	2	AAV15422	Aav15422 Mouse pol
C 31	83.4	3.7	49999	2	AAS23895	Aaz23895 Murine LO
32	83.2	3.7	372	5	AAS75452	Aas75452 DNA encod
33	83	3.7	393	5	AAS90684	Aas90684 DNA encod
34	83	3.7	96596	8	ADA02564	Ada02564 Human RAS
35	83	3.7	96596	9	ADB72302	Adb72302 Human RAS
36	82.6	3.7	309	5	AAS71089	Aas71089 Probe #25
C 37	82.2	3.7	496	4	AAI12609	Aai12609 Human foe
C 38	82.2	3.7	496	4	ABA54309	Aba54309 Human bre
C 39	82.2	3.7	496	4	AAI33960	Aai33960 Probe #26
C 40	82.2	3.7	496	4	ABA43847	Aba43847 Human bre
C 41	82.2	3.7	496	4	ABA44068	Aba24068 Probe #25
C 42	82.2	3.7	496	4	AAK28026	Aak28026 Human bra
C 43	82.2	3.7	496	4	AAK02592	Aak02592 Human liv
C 44	82.2	3.7	496	4	ABS27626	Abs27626 Human liv
C 45	82.2	3.7	496	5	AAI02512	Aai02512 Probe #25

ALIGNMENTS

RESULT 1
AAX23321
ID AAX23321 standard; cDNA; 2226 BP.
XX
AC AAX23321;
XX
DT 11-JUN-1999 (first entry)
XX
DE N. meningitidis strain H44/76 LbpB cDNA.
XX
KW lbpB; lactoferrin binding protein; vaccine; neisserial disease;
KW meningitis; diagnosis; treatment; ds.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
CDS 1..2226
FT /*tag= a
FT /product= "LbpB"
XX
PN WO9909176-A1.
XX
PD 25-FEB-1999.
XX
PF 10-AUG-1998; 98WO-EP005117.
XX
PR 15-AUG-1997; 97GB-00017423.
PR 05-FEB-1998; 98GB-00002544.
XX
PA (UYUT-) RIJXSUNIV UTRECHT.
PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
XX
PI Pettersson-Fernholm AM, Tommassen JPM;
XX
DR WPI; 1999-190165/16.
DR P-PSDB; AAW93494.
XX
PT New lactoferrin-binding protein B polynucleotides - obtained from
PT Neisseria meningitidis, used to develop products for the diagnosis,
PT prevention and treatment of neisserial disease, e.g. meningitis.
XX
PS Claim 2; Page 90-94; 116pp; English.
XX
CC This invention describes novel lactoferrin-binding protein B (lbpB)
CC strains of Neisseria meningitidis. The products of this invention can be
CC used for vaccinating humans against neisserial disease e.g. meningitis.

App. 10/57

CC Antibodies raised against the proteins of the invention can be used for
 CC diagnosing or treating neisserial disease in humans. The lbpB
 CC polypeptides can also be used for identifying compounds which inhibit the
 CC polypeptides

XX Sequence 2226 BP; 683 A; 483 C; 571 G; 489 T; 0 U; 0 Other;

Query Match 100.0%; Score 2226; DB 2; Length 2226;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGTGTAACCGCAATATGCGCGATGCTGCTGTTGCGCCCTACTTTTGGCATCTGTATT	60
Db	1	ATGTGTAACCGCAATATGCGCGATGCTGCTGTTGCGCCCTACTTTTGGCATCTGTATT	60
Qy	61	GGCGCAATTTCCGCGTGCAGCTGTTGTCGAATCAACGCGACCGCGTACCCCGTCAC	120
Db	61	GGCGCAATTTCCGCGTGCAGCTGTTGTCGAATCAACGCGACCGCGTACCCCGTCAC	120
Qy	121	TTCAAGTCTAAGACGTTCCCACTCCGCGCCCTGCGCAACCTTCTATAGAAACACGCGG	180
Db	121	TTCAAGTCTAAGACGTTCCCACTCCGCGCCCTGCGCAACCTTCTATAGAAACACGCGG	180
Qy	181	GTGCGGTCAACCGCGCTCGCTGCGTGCAGCAATGCGGCTGTTGAGCGGATTTTCGCA	240
Db	181	GTGCGGTCAACCGCGCTCGCTGCGTGCAGCAATGCGGCTGTTGAGCGGATTTTCGCA	240
Qy	241	ACTTCTGATAGGTGCGCAATGATTTTCCAAATAGCAAAACAGCAGAAAGAGCTGCG	300
Db	241	ACTTCTGATAGGTGCGCAATGATTTTCCAAATAGCAAAACAGCAGAAAGAGCTGCG	300
Qy	301	TTTAAAGAGGTGATGTTCTGTTTATACGTTTCAAAAAGATAAATTCAGTGGCTT	360
Db	301	TTTAAAGAGGTGATGTTCTGTTTATACGTTTCAAAAAGATAAATTCAGTGGCTT	360
Qy	361	AAGGATAAAATTCATCAACGCAATCCTAATGTAGAAATTAGGACATCAGAAAAATGAAAT	420
Db	361	AAGGATAAAATTCATCAACGCAATCCTAATGTAGAAATTAGGACATCAGAAAAATGAAAT	420
Qy	421	AAAAAATATGTTATGATTTGTGGATGCGGTTATGATATATCTAAAAACGGAACAGAT	480
Db	421	AAAAAATATGTTATGATTTGTGGATGCGGTTATGATATATCTAAAAACGGAACAGAT	480
Qy	481	GAAATTCAGTGGATCTCAAAATCGAAGCAGTTTCTAATCGTTTGGTACGAGCTTTT	540
Db	481	GAAATTCAGTGGATCTCAAAATCGAAGCAGTTTCTAATCGTTTGGTACGAGCTTTT	540
Qy	541	GTATATATTCGGGAGACATCTTCCCAATCTTTTACCGAGCGGGGAAACGGTCAATAT	600
Db	541	GTATATATTCGGGAGACATCTTCCCAATCTTTTACCGAGCGGGGAAACGGTCAATAT	600
Qy	601	TCCGGTAACTGGCAATATATGACCGATGCCATAGTCATCGAAACAGAAACGAGGAT	660
Db	601	TCCGGTAACTGGCAATATATGACCGATGCCATAGTCATCGAAACAGAAACGAGGAT	660
Qy	661	CCTAGCGAAGATTTGGGTATCTCGTTTATACGTTCAAAATGTCGAGCAACTTCTTAT	720
Db	661	CCTAGCGAAGATTTGGGTATCTCGTTTATACGTTCAAAATGTCGAGCAACTTCTTAT	720
Qy	721	GCTGCACTGCGCAGACCGGGAGGAAAAACATCTCGCGAATATACGGTTGATTTCGAT	780
Db	721	GCTGCACTGCGCAGACCGGGAGGAAAAACATCTCGCGAATATACGGTTGATTTCGAT	780
Qy	781	AAGAAAACTTTGACGGGTCAATTAATTAATAATAGTATGTCGCAAAAGAACCGATGAA	840
Db	781	AAGAAAACTTTGACGGGTCAATTAATTAATAATAGTATGTCGCAAAAGAACCGATGAA	840
Qy	841	AAGAAACCACTGACCATTTACGACATTCAGCAATTTGGACGGCAACCGCTTTACCGG	900
Db	841	AAGAAACCACTGACCATTTACGACATTTACGCAATTTGGACGGCAACCGCTTTACCGG	900
Qy	901	AGTGCACAAAGTTTAAACCGAGTTGAAGACGAGCCAGCTGTATTAAGAGCATTTGTTTC	960

Db	901	AGTGCACAAAGTTTAAACCGAGTTGAAGACGAGCCACGCTGATATAAGAGCATTTGTTTTTC	960
Qy	961	CATACCGATCGCGATCAGCGCTTGAGGCGGTTTTTTTCGCGATATAAGGGGAGAGCTT	1020
Db	961	CATACCGATCGCGATCAGCGCTTGAGGCGGTTTTTTTCGCGATATAAGGGGAGAGCTT	1020
Qy	1021	GCGGACGGTTTTATCAGCAACGACAAACAGCGTATTTCGGGTATTTCGAGCAAAAAACA	1080
Db	1021	GCGGACGGTTTTATCAGCAACGACAAACAGCGTATTTCGGGTATTTCGAGCAAAAAACA	1080
Qy	1081	AAGCATCAAAACGACAGATACAAATCTCTGCTATCCGCTCTGAAAAACACCAAAATC	1140
Db	1081	AAGCATCAAAACGACAGATACAAATCTCTGCTATCCGCTCTGAAAAACACCAAAATC	1140
Qy	1141	TTGGAATCTCTGAAAAATTTCCGTTGACGAGCGGACGATATAAAATGCCCCCGCTTGGC	1200
Db	1141	TTGGAATCTCTGAAAAATTTCCGTTGACGAGCGGACGATATAAAATGCCCCCGCTTGGC	1200
Qy	1201	ATTTCCTCTCTGCGGATTTTGGCCATCCCGACAACTCTCTGTCGAGGGCGTGAATTT	1260
Db	1201	ATTTCCTCTCTGCGGATTTTGGCCATCCCGACAACTCTCTGTCGAGGGCGTGAATTT	1260
Qy	1261	CCTTTGGTTAGCAAGAAAAACATCGAGCTTCCGACGCGCAGGAAAAATGACCGTCCGT	1320
Db	1261	CCTTTGGTTAGCAAGAAAAACATCGAGCTTCCGACGCGCAGGAAAAATGACCGTCCGT	1320
Qy	1321	GCTTTGTCGATTTTCTGACCTATGTCAAACTCGACCGATATAAACTGACCGCCACGCA	1380
Db	1321	GCTTTGTCGATTTTCTGACCTATGTCAAACTCGACCGATATAAACTGACCGCCACGCA	1380
Qy	1381	AGTAAACCAAGCGGAAAGATAAAGGAAAGATGAAGAGATACAGCGTGTGTAAGCAC	1440
Db	1381	AGTAAACCAAGCGGAAAGATAAAGGAAAGATGAAGAGATACAGCGTGTGTAAGCAC	1440
Qy	1441	GAAGAGGACGAGAAAGATGAGCGCGCAGAGCGAGCGAGGAGCGAGAAATCGGC	1500
Db	1441	GAAGAGGACGAGAAAGATGAGCGCGCAGAGCGAGCGAGGAGCGAGAAATCGGC	1500
Qy	1501	GATGAAGGAGGAGTGCAGGAGACGAAAGCGCAGAAAAACGAAAGCGCGGAGAGAGAG	1560
Db	1501	GATGAAGGAGGAGTGCAGGAGACGAAAGCGCAGAAAAACGAAAGCGCGGAGAGAGAG	1560
Qy	1561	GCTGAAGAACTCTGAAGAACCCGAAAGAAATTCGCGCGGAGAGCGCGGGTGTGTTCA	1620
Db	1561	GCTGAAGAACTCTGAAGAACCCGAAAGAAATTCGCGCGGAGAGCGCGGGTGTGTTCA	1620
Qy	1621	GACGGCATCTGCGCGCTCGGAGCTCTTAAAGCGAGGATATCGACCTTTTCTGAAA	1680
Db	1621	GACGGCATCTGCGCGCTCGGAGCTCTTAAAGCGAGGATATCGACCTTTTCTGAAA	1680
Qy	1681	GATATCGCAGCGGAGGAGCGACATTCGCAAACTGAAAAAGCAGCTATACCGGCACT	1740
Db	1681	GATATCGCAGCGGAGGAGCGACATTCGCAAACTGAAAAAGCAGCTATACCGGCACT	1740
Qy	1741	TGGGAAGCGGATATCAGCAAAACCCATTCATATGGAACAATCATCGGATATAAAAGCGGCA	1800
Db	1741	TGGGAAGCGGATATCAGCAAAACCCATTCATATGGAACAATCATCGGATATAAAAGCGGCA	1800
Qy	1801	AAAGCAGAAATTTGACGTTGATTTTCGCGAGAAATCGATTTCCGGAACGCTGACGAGAA	1860
Db	1801	AAAGCAGAAATTTGACGTTGATTTTCGCGAGAAATCGATTTCCGGAACGCTGACGAGAA	1860
Qy	1861	AACGCTGTACAACTGCTTTTCCATATTGAAAAACGCGCTGATTGAGGGCAATGGTTCCAC	1920
Db	1861	AACGCTGTACAACTGCTTTTCCATATTGAAAAACGCGCTGATTGAGGGCAATGGTTCCAC	1920
Qy	1921	CGCAGCGGCACTCGGGATAACCGGATCAATCTTTCGGGAAATGATTCGACTAATCTCT	1980
Db	1921	CGCAGCGGCACTCGGGATAACCGGATCAATCTTTCGGGAAATGATTCGACTAATCTCT	1980
Qy	1981	CCAGTTTCAAGGCAATAATCTTCTGTAACAGCGCGCTTTTACGGCCGCGAGCGGAG	2040
Db	1981	CCAGTTTCAAGGCAATAATCTTCTGTAACAGCGCGCTTTTACGGCCGCGAGCGGAG	2040

QY 2041 GAATGGGGGGTACTATTTTCAATATGATGGAATCTCTGGTAACTGAAGTACT 2100
 Db |||||
 QY 2041 GAATGGGGGGTACTATTTTCAATATGATGGAATCTCTGGTAACTGAAGTACT 2100
 Db |||||
 QY 2101 GAAATGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 2160
 Db |||||
 QY 2101 GAAATGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 2160
 Db |||||
 QY 2161 GAAATGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 2220
 Db |||||
 QY 2161 GAAATGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 2220
 Db |||||
 QY 2221 AATATGA 2226
 Db |||||
 QY 2221 AATATGA 2226
 Db |||||

RESULT 2
 ID ACA41945 standard; DNA; 2226 BP.
 AC ACA41945;
 XX 19-JUN-2003 (first entry)
 XX Prokaryotic essential gene #21602.
 XX Antisense; ds; prokaryotic essential gene; cell proliferation;
 XX drug design; gene.
 XX Neisseria meningitidis.
 XX W0200277183-A2.
 XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107
 XX 21-MAR-2001; 2001US-00915242.
 XX 06-SEP-2001; 2001US-00948953.
 XX 25-OCT-2001; 2001US-0342943P.
 XX 08-FEB-2002; 2002US-00972851.
 XX 06-MAR-2002; 2002US-0342659P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 XX P-PSDB; ABU38075.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 Claim 14; SEQ ID NO 29815; 1766pp; English.
 The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *X. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 2226 BP; 701 A; 466 C; 566 G; 493 T; 0 U; 0 Other;
 Query Match 79.7%; Score 1774.8; DB 7; Length 2226;
 Best Local Similarity 88.4%; Pred. No. 0;
 Matches 1990; Conservative 0; Mismatches 212; Indels 48; Gaps 4;
 QY 1 ATGTGTAACCGAATTATGGCGCAATGTCTTGTGGCCCTTACTTTTGGCACTTTGATT 60
 Db 1 ATGTGTAACCGAATTATGGCGCAATGTCTTGTGGCCCTTACTTTTGGCACTTTGATT 60
 QY 61 GGCGGCAATTCGGCGTGCAGCTGTGTGCAATCAACGCGGACCGGTACCCGTCAC 120
 Db 61 GGCGGCAATTCGGCGTGCAGCTGTGTGCAATCAACGCGGACCGGTACCCGTCAC 120
 QY 121 TTCAAGTCTAAGGACGTTCCCACTCCGCCCTCCCAACCTCTATAGAACACCGCG 180
 Db 121 TTCAAGTCTAAGGACGTTCCCACTCCGCCCTCCCAACCTCTATAGAACACCGCG 180
 QY 181 GTGCCGTCAACCGGCGCTGCGTGGCGCAATCGGCTGTGTAGCGGCAATTTGCGCA 240
 Db 181 GT-----CAACCGCGCGCGCTGCGTGGCGCAATCGGCTGTGTAGCGGCAATTTGCGCA 240
 QY 241 ACITCTGATAGTTGGCAATGATTTTCCAAATAGCAAAACAGCAGAGAAAGCTGTG 300
 Db 235 TTTTCATCGTGAAGATGCGACGCGCAATTCGCGATAGCAAAACAGCAGAGAAAGCTGTG 294
 QY 301 TTTAAGAGAGTGTCTCTGTTTATACGTTTCAAAAAGATAAATCTTCACTGGCTT 360
 Db 295 TTTAAGAGAGTGTCTCTGTTTATACGTTTCAAAAAGATAAATCTTCACTGGCTT 354
 QY 361 AAGGATAAAATTCATCAACGCAATCTCTATGTAGAAATAGGACATCAGAAAATGAAAAT 420
 Db 355 AAGGATAAAATTCATCAACGCAATCTCTATGTAGAAATAGGACATCAGAAAATGAAAAT 414
 QY 421 AAAAAATATGTTATGAATTTGATGCGGTCGCGTATGTATATATATATATATATATATAT 480
 Db 415 AAAAAATATGTTATGAATTTGATGCGGTCGCGTATGTATATATATATATATATATATAT 474
 QY 481 GAAATAGTGGACTTCAAAATCGAAGCAATCTCTAATCGTTTTCGCTACGACGTTT 540
 Db 475 GAAATAGTGGACTTCAAAATCGAAGCAATCTCTAATCGTTTTCGCTACGACGTTT 534
 QY 541 GTATATATTCGGAGAAATCTTCCCAATCTTTTACCGAGCGCGGGAACGGTCAATAT 600
 Db 535 GTATATATTCGGAGAAATCTTCCCAATCTTTTACCGAGCGCGGGAACGGTCAATAT 594
 QY 601 TCGGTAACTGCAATATATGACCGTGCATCGTATCGAATAGGACATCAGAAAATGAAAAT 660
 Db 595 TCGGCAATCTGCAATATATGACCGTGCATCGTATCGAATAGGACATCAGAAAATGAAAAT 654
 QY 661 CTAGCGAAGATTTGGGTTATCTCGTTTATACGTTCAAAAATGCGGACCACTTCTTAT 720
 Db 655 CTAGCGAAGATTTGGGTTATCTCGTTTATACGTTCAAAAATGCGGACCACTTCTTAT 714
 QY 721 GCTGCGACTGCGCAGCAGCGGAGGAAACATCTCTCCGCAATATACGGTTGATTTTCGAT 780

715 GCTGCGACTCCGACGACGAGGAGAAACATCTCCGCAATATACGCTAGATTTCGGT 774
781 AAGAAACTTTGACGGCTCAATTAATTAATAATCAGTATGTGCAAAAGAAACCGATGAA 840
775 AAGAAACTTTGACGGCTCAATTAATTAATAATCAGTATGTGCAAAAGAAACCGATGAA 834
841 AAGAAACCATGACCATTTAGACATTAACGACATTTGACGCGACACCGCTTTACCGGC 900
835 AAGAAACCGCTGACCATTTAGACATTTACTGCAACATTTGACGCGCAACCGCTTTACCGGC 894
901 AGTGCCAAAGTTAACAACCGAGTTGAAGACGACGACGCTGATAAAGAGCATTTGTTTTTC 960
895 AGTGCCAAAGTTAACAACCGAGTTGAAGACGACGACGCTGATAAAGAGCATTTGTTTTTC 954
961 CATACCGATGCGATCAGCGCTTTGAGGCGGTTTTTTTCGCGATAGAGGGAAGAGCTT 1020
955 CATACCGATGCGATCAGCGCTTTGAGGCGGTTTTTTTCGCGATAGAGGGAAGAGCTT 1014
1021 GCCGACGCTTTATCAGCAACGACCAACAGCGTATTTCCGCTATTTCCGAGCA---AAAA 1077
1015 GCCGACGCTTTATCAGCAACGACCAACAGCGTATTTCCGCTATTTCCGAGCAACAAAA 1074
1078 ACAAACGATCAAAACGACGACATCAAAATCCTGCTATGCGCTCTGAAAAACACACCAAA 1137
1075 ACAGACGATCAAAACGACGATCAAAATCCTGCTATGCGCTCTGAAAAACACACCAAA 1134
1138 ATCTTGATCTCTGAAAAATTTCCGTTGACGAGGACGATATAAAATGCGCGCGCTTT 1197
1135 ATCTTGATCTCTGAAAAATTTCCGTTGACGAGGACGATGATAGCAATGCGCGCTTT 1194
1198 GCCATTTCCCTCTGCGCGATTTGGCCATCCGACCAACCTCTGTCGAAGGGCGTGAA 1257
1195 GCCATTTCCCTCTGCGCGATTTGGCTATCCCGCAAACTCTTGTGCAAGGGCGTGAA 1254
1258 ATTCCTTTGGTTAGCCAGAGAAACCATCGAGCTTGCCGACGCGGACGAGAAATGACCGTC 1317
1255 ATCTCTTGCTCAAGTACTCAAAACCATCGATCTTCCGACGCGGACGAGAAATGACCGTC 1314
1318 CGTGCTTTGCGATTTTCTGACCTATGTGAACTCGGACGAGTAATACTGACCGCCA 1377
1315 AGTGCTTTGCGATTTTCTGACCTATGTGAACTCGGACGAGTAATACTGACCGCCA 1374
1378 GCAAGTAAACCAAGGCGGAGATAAA-----GGGAAGCATGAA 1416
1375 GCAAGTAAACCAAGGCGGAGATAAAATTCGGAAGATGAAATTTGGTGAAGCGAGAA 1434
1417 GAGGATACAGGCGTTGGTAAACGACGAAGAGCGACGAGATGAAGCCGACGAGGCGAC 1476
1435 AATGAGAGGATTTGTCGCTGAAGAGAAACACGAGAGACGAAGTCTGAGAGATGAA 1494
1477 GAAGGAGCGAGACGAATCGCGATGAAGAGAGGAGTGCGGAAGACGAGACCGCAGAA 1536
1495 GACAGAGAGAGACGAAGTTTCCGAAGATGTAACAGTGAAGACGAGAGAGAAATCGCC 1554
1537 AACGAGGCGGCGAGAGACGAAGCTGAAGACCTGAAGACCCGAGAGAAATCGCG 1596
1555 GAAGAAGATGATGAAGCGGAGAGGAGGAGTTGAAGACCCGAGAGAAATCGCG 1614
1597 GCAGAAGCGGCGGTTGGTTTTCAGACGCGATCTTCCGCGCTCCGGAAGCTCTAAAGC 1656
1615 GAAGAAGCGGCGGTTGCGGTTTCAGACGCGATCTTCCGCGCTCCGGAAGCTCTAAAGC 1674
1657 AGGATATGACCTTTCTGAAAGGATTCGACGCGGAGACGACATTCGCAACT 1716
1675 AGGACATGACCTTTCTGAAAGGATTCGACGCGGAGACGACATTCGCAACT 1734
1717 GGAAGACGACGATACCGGCACTTTGGGAGCGGATATCAGCAAAACCCATTCATGGGAC 1776
1735 GGAAGACGACGATACCGGCACTTTGGGAGCGGATATCAGCAAAACCCATTCATGGGAT 1794
1777 AATCATGCGGATATAAAGCGCAAGCAGAAATTTGACCTTGAATTCGCGGAGAAATCG 1836

1795 AATAAGCGCGATAAAAAAGCGCAAAAGCAGAAATTTGACGTTGATTTTCGCGAGAAATCG 1854
1837 ATTTCCGAGCGCTGACGAGAAACCGGTGTCAACCTGCTTTCCATATTTGAAAAACGGC 1896
1855 ATTTCCGAGCGCTGACGAGAAACCGGTGTGAGAGCTGCTTTCTATATTTGAAAAAGGT 1914
1897 GTGATTTAGCGCAATGTTTCCACGCGACAGCGCGCACTCGGGATAACGGCATCAATCTT 1956
1915 GTGATTTAGCGCAATGTTTCCACGCGACAGCGCACTCGGGATAACGGCATCAATCTT 1974
1957 TCGGGAATGATTCGATTAATCTCTCCAAAGTTTAAAGCCAAATATCTTCTTTGACAGGC 2016
1975 TCGGGAATGATTCGATTAATCTCTCCAAAGTTTAAAGCCAAATATCTTCTTTGACAGGC 2034
2017 GGCTTTTACGCGCGGAGCGGAGGATTCGGCGGTACTATTTTCAATTAATGATGGGAAA 2076
2035 GGATTTTACGCGCGGAGCGGAGGATTCGGCGGTACTATTTTCAATTAATGATGGGAAA 2094
2077 TCTCTTGATATACTGAAGATACTGAAAAATGAAGCTGAAGCTGAAGTTGAAAAATGAAGCT 2136
2095 TCTCTTGATATACTGAAGATATTGACAA-----TGAATTTGAAGCT 2136
2137 GGTGTTTCCGCAACGATTAACACCTGAAGCTAAACCCCAATTCGCGGTGATTCGCTCG 2196
2137 GATGTTTCCGCAACGATTAACACCTGAAGCTAAACCCCAATTCGCGGTGATTCGCTCG 2196
2197 AAGAAAGATATAAGAGGTGGAATAATGA 2226
2197 AAAAAAGATATGAGGAGGTGGAATAATGA 2226

RESULT 3
AA23323
ID AA23323 standard; cdna; 2124 BP.
XX
AC AA23323;
XX
DT 11-JUN-1999 (first entry)
XX
DE N. meningitidis strain 881607 LbpB cdna.
XX
LbpB; lactoferrin binding protein; vaccine; neisserial disease;
KW meningitis; diagnosis; treatment; ds.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
CDS 1..2124
/*tag= a
/product= "LbpB"
XX
FN WO9909176-A1.
XX
PD 25-FEB-1999.
XX
PF 10-AUG-1998; 98WO-EP005117.
XX
PR 15-AUG-1997; 97GB-00017423.
PR 05-FEB-1998; 98GB-00002544.
XX
XX (UYUT-) RIJKSUNIV UTRECHT.
(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
XX
XX Pettersson-Fernholm AM, Tommassen JPM;
XX
XX WPI; 1999-190165/16.
XX
XX P-PSDB; AAW93496.

New lactoferrin-binding protein B polynucleotides - obtained from
PT Neisseria meningitidis, used to develop products for the diagnosis,
PT prevention and treatment of neisserial disease, e.g. meningitis.
XX
XX Claim 2; Page 105-109; 116pp; English.

Ad. cat

XX This invention describes novel lactoferrin-binding protein B (LbpB) strains of *Neisseria meningitidis*. The products of this invention can be used for vaccinating humans against neisserial disease e.g. meningitis. CC Antibodies raised against the proteins of the invention can be used for CC diagnosing or treating neisserial disease in humans. The LbpB CC polypeptides can also be used for identifying compounds which inhibit the CC polypeptides

XX
SQ Sequence 2124 BP; 663 A; 461 C; 541 G; 459 T; 0 U; 0 Other;

Query Match 67.4%; Score 1499.8; DB 2; Length 2124;
Best Local Similarity 83.3%; Pred. No. 0;
Matches 1779; Conservative 0; Mismatches 317; Indels 39; Gaps 5;

QY 1 ATGTGTAACCGAATATGGCGGCAATGTCTTGTGGCCCTTACTTTTGGCACTTTGTATT 60
DB 1 ATGTGTAACCGAATATGGCGGCAATGTCTTGTGGCCCTTACTTTTGGCACTTTGCATC 60

QY 61 GGCGCAATTTCCGGGTGCGAGCTGTGTGCAATCAAGCCGACCGCGTACCCGTCAT 120
DB 61 GGCGCAATTTCCGGGTGCGAGCTGTGTGCAATCAAGCCGACCGCGTACCCGTCAT 120

QY 121 TTCAAGTCTAAGGAGCTTTCCCACTCCGCCCTCGCCAAACCTTCTATAGAAACCAACGCG 180
DB 121 TTCAAGTCTAAGGAGCTTTCCCACTTCGCTCTCTGCGGGTCTTCGGTAGAAACCAACGCG 180

QY 181 GTGCGGTCAACCGGCGCTCGCGTGTGGTGGCAATGCGGCTGTGAGCGGATTTTCGCA 240
DB 181 GT-----CAACCGGACCGCGCTGTGGTGGCAATGCGGCTGTGAGCGGATTTTCGCA 240

QY 241 ACTTCTGATAAGGTGGCAATGATTTTCCAAATAGCAACAGCAGAGAAAGCTGTGCG 300
DB 241 ACTTCTGATAAGGTGGCAATGATTTTCCAAATAGCAACAGCAGAGAAAGCTGTGCG 300

QY 301 TTTAAGAGGTGATGTTCTGTTTTTATACGGTTTCAAAAAAGATAAACTTCAGTGGCTT 360
DB 295 TTTAAGAGGAGATATCTCTGTTTATACGGTTTCCAAANAAGATCAACGTACGAGCTT 354

QY 361 AAGATATAATTCATCAACGCAATCTTATGAAATATAGCAATACGAAATGAAAT 420
DB 355 AAGATATAATTCGTCACCAATCTTACGCAAGCAATACCAATCGGAAAGAAAT 414

QY 421 AAAAAATATGTTATGAATTTGCGATGCGGTTATGTATATATCTTAAACGAGACAT 480
DB 415 AAAAAATATGAATTTTGTAGATGCGATTATGTATATATCTTAAAGACGGAAGAT 474

QY 481 GAAATGAGTGGACTTCAAAATCGCAAGCTTTTCTAATCGTTTGTGCTACGAGCTTT 540
DB 475 GAAATGAGTGGACTTCAAAATTAACAGCAGTCTACCAACCGTTTGTGTATGACGTTT 534

QY 541 GTATATTTTCCGGAGAACATCTTCCCAATCTTTACGAGCGCGGAAACGTTGCAATAT 600
DB 535 GTATATTTTCCGGAGAACATCTTCCCAATCTTTTACGAGCGCGGAAACGTTGCAATAT 594

QY 601 TCCGTAACCTGGCAATATATGACGATGCGATGCTATCGAATGTCGAGCAATCTTCTAT 660
DB 595 TCCGTAACCTGGCAATATATGACGATGCGATGCTATCGAATGTCGAGCAATGTCGAT 654

QY 661 CTTAGCAAGATTGGGTATCTCGTTTATTAGCGTCAAAATGTGAGCAATCTTCTAT 720
DB 655 CTTAGCAAGATTGGGTATCTCGTTTATTAGCGTCAAAATGTGAGCAATCTTCTAT 714

QY 721 GCTGCGACTCCGACGACCGGAGGGAACATCTCTGCGCAATATACGTTGATTTTCGAT 780
DB 715 GCTGCGACTCCGACGACCGGAGGGAACATCTCTGCGCAATATACGTTGATTTTCGAT 774

QY 781 AAAAAATTTGAGCGGTCAATTAATTAATAATCAGTATCTGCAAAAGAAACCGATGAA 840
DB 775 CAAAAAATCTGATGGCAAGCTGATTAATAATCAGTATCTGCAAAAGAGATGATCTCT 834

QY 841 AAAAAACCACTGACATTTACGACATTTACGCAACATTTGACGCGCAACCGCTTTACCGC 900
DB |||||

DB 835 AAAAAACCACTGACCATTTTACGACATTTACTGCAAAATTTGACGCGCAACCGCTTTACCGGC 894

QY 901 AGTGGCAAAATTTAAACACCGAGTTGAAGACGACCGCACTGTAAGAGAGCATTTGTTTTTC 960

DB 895 AGTGGCAAAATTTAAACACCGAGTTGAAGAGCAATCAACGCTGATAAAGAAATTTGTTTTTC 954

QY 961 CATACCGATGCGCATCAGCGGCTTGGAGGCGGTTTTTTTTCGGCGATAAGGGGGAAGAGCTT 1020

DB 955 CATACCGATGCGCATCAGCGGCTTGGAGGCGGTTTTTTTTCGGCGATAAGGGGGAAGAGCTT 1014

QY 1021 GCGGACCGTTTTATCAGCAACGACAGCGATTTTCGGCGTATTCGAGCA---AAAAA 1077

DB 1015 GCGGACCGTTTTATCAGCAACGACAGCGATTTTCGGCGTATTCGAGCAACAAAAA 1074

QY 1078 ACACACCGCATCAACCGCAGCAGATACAAATCTCTGCTATGCGCTCTGMAAAACACACCAA 1137

DB 1075 ACAGAGACAGCAACGCAATCAGATACAAATCTCTGCGCTCTGMAAAACACACCAA 1134

QY 1138 ATCTTGGATTTCTGAAAAATTTTCGTTGACGAGCGCAGGATATAAAATGCGCGCGCTTT 1197

DB 1135 ATCTTGGATTTCTGAAAAATTTTCGTTGACGAGCAAGTGTGAAATTCGCGACCGTTT 1194

QY 1198 GCCATTTCCCTCTGCGCGATTTTGGCCATCCCGCAAACTCTTGTTCGAAAGGCGTGA 1257

DB 1195 GAGGTTTCCATATGCCCGATTTTGGTCATCCCGCAAACTCTTGTTCGAAAGGCGTGA 1254

QY 1258 ATTCTTTGGTTAGCAAGAGAAAAACCATCTGAGCTTCCGACGCGCAGGAAATGACCGTC 1317

DB 1255 ATTCTTTGGTTAGCAAGAGAAAAACCATCTGAGCTTCCGACGCGCAGGAAATGACCGTC 1314

QY 1318 CGTCTTGTTCGACTTTTTCGACCTATGTGAACTCTCGACGGAATAAACTGACCGCCA 1377

DB 1315 CGTCTTGTTCGACTTTTTCGACCTATGTGAACTCTCGACGGAATAAACTGACCGCCA 1374

QY 1378 GCAAGTAAACCAAGGCGGAGATTAAGGAGAGATGAAGAGATACAGCGTTTGGTAAAC 1437

DB 1375 GCGTCCAAACGGAAGGCGGAGATGAAGAGGAGGAGCAAGAGGCTGTAGGCGTTGATAAC 1434

QY 1438 GACCAAGAGCAGCGGAGATGAGCGCGCAGAGGAGCGAGCAGGAGCGGAGCAATC 1497

DB 1435 GGTAAAGAGCAGAGAGCAATCGCGATGAAGAGACCCGAGAGCAAGTCTGTAGAA 1494

QY 1498 GCGGATGAAGAGGAGGTGCGGAGACGAAACCGCAGAAACGAAAGCGCGCAAGAGAC 1557

DB 1495 GATGAACGCAAGATGAAGACGAAAGAAATCGAAGAA-----GAACCTGAA 1542

QY 1558 GAAGCTGAAGAACTTGAAGAACCGGAGAGATCGCGCGCAGAGCGCGGCGTGTGTT 1617

DB 1543 GAAGAGCTGAAGAGGAGAAACCGGAGAGAAATTCGCGCAGAAAGCAACGCGCGT 1602

QY 1618 TCAGACGCGATCTCTGCGCGCTCCGGAAGCTCTTAAAGGAGGAGGATTCGACCTTTTCTG 1677

DB 1603 TCAGGCGAGCATCTGCGCCACTCCGGAAGCTCTTAAAGGAGGAGCATTCGACCTTTTCTG 1662

QY 1678 AAGGTATTCGACGCGGAGCGGACCTTCGCAAACTGGAAAAAGCAGCTATACCGGC 1737

DB 1663 AAGGTATTCGACGCGGAGCGGACCTTCGCAAACTGGAAAAAGCAGCTATACCGGC 1722

QY 1738 ACTTGGAGAGCGGTATCAGCAAC-----CAATTCATGGGCAATCAT 1782

DB 1723 ACTTGGAGAGCGGTATCAGCAAC-----CAATTCATGGGCAATCAT 1782

QY 1783 GCGGATAAAAAGCGGCAAAAGCAGAAATTTGAGTTGATTTTCGCGCAGAAATCGATTTC 1842

DB 1783 GCG---AATCAAGGGCAAAAGCAGAAATTTACGTTGATTTTGAAGCGAGGCGGTGCTC 1839

QY 1843 GGAACCTGACGAGAAAAAACCGTGTACAACTGCTTTCCATATTTGAAAAACGCGGTGATT 1902

DB 1840 GGAATGCTGACAGAAAAAAATGATACAAACCCCGCTTTTATATTTGAAAAAGGTGATT 1899

QY 1903 GAGGCAATGTTTTCACGCGACGCGCACTCGGAGTAAACGCGCATCAATCTTTTCGGGA 1962

DB 1900 GACGCTAACGCTTTTCACGCTTTTGGCGCATACTCGGAGAACGCGTATTGACCTTTTCGG 1959

QY 1963 AATGATTCGACTAATCTCCAGTTTCAAAGCCCAATATCTTCTTTGTAACAGGGCGCTTT 2022
Db 1960 CAGGTTTCGACTAACCCGGAAGAACTTCAAAGCCGACAATCTTCTTTGTAACAGGGCGCTTT 2019
QY 2023 TACGGCCGACAGGCGGAGGAACTTGGCGGTACTATTTTCAATAATGATGGAAATCTCTT 2082
Db 2020 TATGCGCCGACAGGCGGAGAACTTGGCGGTAAATATATCGACGCGACCGGAAATTCGTT 2079
QY 2083 GGTATAACTGAAGATACCTGAAATCAAGCTCAAGC 2117
Db 2080 GCGGTATTTGGCGGCAAAAAGATGACAGGAGGC 2114

RESULT 4
AAX23319
ID AAX23319 standard; cDNA; 2277 BP.
AC AAX23319;
DT 11-JUN-1999 (first entry)
DE N. meningitidis strain BNCV LbpB cDNA.
KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
KW meningitis; diagnosis; treatment; ds.
OS Neisseria meningitidis.

Key Location/Qualifiers
FT CDS 100..2277
FT /tag= a
FT /product= "LbpB"
XX WO9909176-A1.
XX 25-FEB-1999.
XX 10-AUG-1999; 98WO-EP005117.
XX 15-AUG-1997; 97GB-00017423.
XX 05-FEB-1998; 98GB-00002544.
XX (UYUT-) RIJKSUNIV UTRECHT.
XX (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
XX Pettersson-Fernholm AM, Tommassen JPM;
XX WPI: 1999-190165/16.
XX P-FSDB; AAW93492.

XX New lactoferrin-binding protein B polynucleotides - obtained from
XX Neisseria meningitidis, used to develop products for the diagnosis,
XX prevention and treatment of neisserial disease, e.g. meningitis.
XX Claim 2; Page 74-78; 116pp; English.
XX This invention describes novel lactoferrin-binding protein B (LbpB)
XX strains of Neisseria meningitidis. The products of this invention can be
XX used for vaccinating humans against neisserial disease e.g. meningitis.
XX Antibodies raised against the proteins of the invention can be used for
XX diagnosing or treating neisserial disease in humans. The LbpB
XX polypeptides can also be used for identifying compounds which inhibit the
XX polypeptides
XX Sequence 2277 BP; 700 A; 469 C; 573 G; 535 T; 0 U; 0 Other;

Query Match 66.9%; Score 1490.2; DB 2; Length 2277;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 1859; Conservative 0; Mismatches 298; Indels 90; Gaps 10;
QY 1 ATGCTAAACCGAATTATGGCGGCAATGCTTCTTGGCCCTTACTTTGGCATCTTGTATT 60
|||||

Db 100 ATGCTAAACCGAATTATGCGGCAATGCTTCTTGTGCCCTTACTTTTGGCAATCTGTATC 159
QY 61 GCGGCAATTTCCGCGTGCAGCCTGTGTGCGAATCAACGCGACCGCGTACCCGCTCACT 120
Db 160 GCGGCAATTTCCGCGTGCAGCCTGTGTGCGAATCAACGCGACCGCGTACCCGCTCACT 219
QY 121 TTCAAGTCTAAGGACGTTCCCACTCCGCCCTCCCAACCTTCTATAGAAACCAACGCG 180
Db 220 TTCAAGTCTAAGGACGTTCCCACTCCGCCCTCCCAACCTTCTATAGAAATCAGCGC 279
QY 181 GTGCCGTCAACCGGCTCGCGTGCAGCAATGCGGCTGTGTGAGGCGCAATTTCCGA 240
Db 280 GT-----CAACCGGCGCGCGTGCAGCAATGCGGCTGCAGGCGGAATACTCTCT 333
QY 241 ACTTCTGATTAAGGTTGGCAATGATTTTCCAAATAGCAAAACAGCAGAGAAAGCTGCG 300
Db 334 TTTTCATCGTGAAGATGGCAGAAATTTCCAAATAGCAAAACAGCAGAGAAAGCTGCG 393
QY 301 TTTTAAAGAAGGTGATGTTCTGTTTTTATACGGTTTCAAAAAAGATAAATCTTCACTG 360
Db 394 TTTTCAAGAAGGTGATGTTCTGTTTTTATACGGTTTCAAAAAAGATAAATCTTCACT 453
QY 361 AAGGATAAATTCATCAACGCAATCTTAATCTAGAAATTTAGGACATCAGAAATGAAAT 420
Db 454 AAAAGCGAAATTTCAAAACGATTTCCGATGTAGAAATTTAGGACATCAGAAAGAAAT 513
QY 421 AAAAATATGTTATGAATTTTGTGATGCGCGTTATGTATATATCTTAAAAAACGAA 480
Db 514 AAAAATATGATTAATTAATTTTGTAGTGCAGTTATGTATA---TGTAAAGGAAAGAT 570
QY 481 GAAATTTGAGTGGACTTCAAATCGCAAGCAGTTTCTAATCGTTTGTGGTAGACGGTTTT 540
Db 571 GAAATTTGAGTGGACTTCAAATCGCAAGCAGTTTCTAATCGTTTGTGGTAGACGGTTTT 630
QY 541 GTATATTTATCCGGAGAACATCTTCCCAATCTTTACCGAGCGGGACGGTCAATAT 600
Db 631 GTATATTTATCCGGAGAACATCTTCCCAATCTTTACCGAGTGGGGACGGTGGAAAT 690
QY 601 TCCGTAATCGCATATATGACCGATGCGCATCTCATCGAAACAGAGAAACAGAGAT 660
Db 691 TCTGTAATCGCATATATGACCGATGCGCATCTCATCGAGCAGGTAAAGC---GGTT 747
QY 661 CTTAGCGAAGATTTGGGTTATCTCGTTTATACGGTCAAAATGTCTGGAGCAATCTTCT 720
Db 748 GGCATTGACAAATTTGGGTTATTTACACATTTTATGTTAAACGATGTTGGTCAACTTCT 807
QY 721 GCTGCGACTGCGACGACGCGGAGGAAACATCTGCGCATATATACGTTTCATTTCCGAT 780
Db 808 GCGGCTAAGGATGTCGACGAAAGGAAACATCTGCTAAATATACGTTAGATTTCGTT 867
QY 781 AAGAAACCTTTGACGGGTCAATTAATTAATAATCAGTATGTGCAAAAGAAACCGATGAA 840
Db 868 AACAAACCTTACGCGGCGAGCTGATTAATAACCAATATGT---CAACCCAGTGAGAG 924
QY 841 AAGAAACCACTGACCATTTACGCAATTCACCGCAATTTGGACGCGCAACCGCTTTAC 900
Db 925 CAAAAACCGCTGACCATTTACCAACATCTGCGCATTTTAAACGCGCAACCGCTTTAC 984
QY 901 AGTGCACAAAGTTAAACCGAGTTGAAGACGCGCACTGATATAAGAGCATTTGTTTTC 960
Db 985 AGTGCACAAAGTTCAATCTGATTTAGGAAAGCCATGCCAATAGAGGACATTTGTTTTC 1044
QY 961 CATACCGATGCGCATCAGCGGCTTGAAGGCGGTTTTTTCGGCATTAAGGGGGAAGCTT 1020
Db 1045 CATGCGCATGCGCATCAGCGGCTTGAAGGCGGTTTTTTCGGCATTAAGGGGGAAGCTT 1104
QY 1021 GCGGACGTTTATCAGCAACGACATCAGCGTATTCGGCGTATTCGACGCAAAACAA 1080
Db 1105 GCGGACGTTTATCAGCAACGACATCAGCGTATTCGGGTATTCGACGCAAAACAA 1160
QY 1081 AAGCATCAACGACGACGATCAAAATCTGCTATCGCTCTGAAACCAACACCAAAATC 1140
Db 1161 -----AAATAGCCCGCTGCGTCTGGAACACACACCAAAATC 1197

1141 TTGGATTCTCTGAAATTTTCGTTGACGAGCGACGATATAAATATGCGCCCGTTGGC 1200
Db |||||
1198 TTGGATTCTCTGAAATTTTCGTTGATGAGCGAAGTGGTGAATATCCCGACCGTTGGC 1257
Qy |||||
1201 ATTTCCTCTGCGCCGATTTTGGCCATCCCGACAAATCTCTTGTGCGAAGGGCGTGAAT 1260
Db |||||
1258 ATTTCCTCTGCGCCGATTTTGGTCAATCCCGACAAATCTTGTGCGAAGGGCATGAAT 1317
Qy |||||
1261 CTTTGGTTAGCCAGAGAAACCATCGAGCTTGGCGAGCGAGGAAATGACCGTCCGT 1320
Db |||||
1318 CTTTGGTTAGCCAGAGAAACCATCGAGCTTGGCGAGCGAGGAAATGACCGTCCGT 1377
Qy |||||
1321 GCTTGTGCGATTTTCTGACCTATGTGAATCTCGAGCGATATAAATCTGACCGCCAGCA 1380
Db |||||
1378 GCTTGTGCGATTTTGTGACCTATGTGAATCTCGAGCGATATAAATCCGACCGCCGCG 1437
Qy |||||
1381 AGTAAACCAAGCGCGAAGATATAAGGGAAGAGTGAAGAGATACAGCGCTTGTACGAC 1440
Db |||||
1438 GCCAAACCGAAGC-----GCAGGACGAGAGATTCCGACATTGATATGGC 1485
Qy |||||
1441 GAAGAGGACCGGAGATGAACCGCGACAGGCGAGGAGGCGGAGCAAGAAATCGGC 1500
Db |||||
1486 GAAGAAAGC---GAAGACGAATCGCGATGAAGAGAGGACCGAGATCGACCGCA 1542
Qy |||||
1501 GATGAAGAGGAGTGGCGAAGCAAGCGCGAGAAATCGCGGAGAGGCGGCGTGTCTCA 1620
Db |||||
1543 GGAGATGAAGCAGCGAAGAGCAAGAGCCACAGAAACGAAGACGGCGAAGAACGAA 1602
Qy |||||
1561 GCTGAAGAACCTGAAGAACCCGGAAGAAATCGCGGAGAGGCGGCGTGTCTCA 1620
Db |||||
1603 GCTGAAGAACCT-----GAAGAGAAATCGTGGCAGAGGCAAC---GGCAGTTCA 1650
Qy |||||
1621 GACGCAATCTGCGCTCGGAGACTCTTAAGCGAGGATATCGACTTTTCTGAAA 1680
Db |||||
1651 AACGCCATCTGCTGCTCGGAGACCTCTAAAGCGAGGATATCGACTTTTCTGAAA 1710
Qy |||||
1681 GGTATCCGACGCGGAGAGCGACATTCGCGAACTGGAAGACGCTATACCGGCACT 1740
Db |||||
1711 GGTATCCGACGCGGAGAGAGATATTCGCGAACTGGAAGACGCTATACCGGCACT 1770
Qy |||||
1741 TGGGAAGCGGTATCAGCAAAACCCATTCATGGGACAAATCATGGGATAAAGAGCGCA 1800
Db |||||
1771 TGGGAAGCGGTATCGGCAAAACCCATTCATGGGACAAATCATGGGATAAAGAGCGCA 1830
Qy |||||
1801 AAACGAGAAATTTGAGTTGATTTGCGGAGAAATCGATTCGGAACGCTGACGGAGAA 1860
Db |||||
1831 AAACGAGTAATTTACCGTTGATTTGCGCAAGAAATCGATTTCCGGAACGCTGACGGAGAA 1890
Qy |||||
1861 AACGGTGTACAACTGCTTTCCATATTAAGAAACGGCGTATGAGGCAATGGTTCCAC 1920
Db |||||
1891 AACGGTGTAGAACTGCTTTCCGTAATTAAGAAACGGCGTATGAGGCAACGGTTCCAT 1950
Qy |||||
1921 GCGACAGCGCACTCGGATTAACGGCAATCAATCTTTCGGAAATGATTCGACTAATCCT 1980
Db |||||
1951 GCGACAGCGCACTCGGATTAACGGCAATCGAATCTTTCGGGCGAGGTTGACCAAACCG 2010
Qy |||||
1981 CCAAGTTTCAAGCAATATCTTCTTGTAAACAGCGCTTTTACGCGCCGCGAGCGGAG 2040
Db |||||
2011 CAGATCTTCAAGCAATATGATCTTCTGTAAGAGGAGATTTTACGCGCCGCGAGCGGAG 2070
Qy |||||
2041 GAATTTGGCGGTACTATTTTCAATAATGATGGGAATCTCTTGTATTAATCTGAAGTACT 2100
Db |||||
2071 GAATTTGGCGGTATTTTCAATAATGATGGGAATCTCTTGTATTAATCTGAAGTACT 2130
Qy |||||
2101 GAAATGAAGCTGAAGCTGAAGTTGAAATGAAGCTGCTGCT----- 2141
Db |||||
2131 GAAATAAAGTTGAAGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGCT 2190
Qy |||||
2142 --TGGCGAAGCTGAAGCTGAAGTAAACCCCAATTCGGCGGTGTTTTCGGTGGCGAAG 2199
Db |||||
2191 GATGTTGAACAGTTAAACCTGAAGTTAAACCCCAATTCGGCGGTGTTTTCGGTGGCGAAG 2250

QY 2200 AAAGATAATAAAGAGGTGGAATAATGA 2226
Db |||||
2251 AAAGATAATAAAGAGGTGGAATAATGA 2277

RESULT 5

AA81489_1/c

Continuation (2 of 9) of AA81489 from base 100001 (N. meningitidis partial DNA sequence)
WP Sequence split into 9 fragments LOCUS AA81489 Accession Aa81489

Fragment Name	Begin	End
WP AA81489_0	100001	110000
WP AA81489_1	210000	210000
WP AA81489_2	200001	310000
WP AA81489_3	300001	410000
WP AA81489_4	400001	510000
WP AA81489_5	500001	610000
WP AA81489_6	600001	710000
WP AA81489_7	700001	810000
WP AA81489_8	800001	837096

Query Match

Best Local Similarity 66.4%; Score 1477.2; DB 3; Length 110000;

Matches 1832; Conservative 81.4%; Pred No. 0;

Mismatches 0; Gaps 8;

QY 1 ATGTAAACCGAATTTATGGCGCATTTCTTGTGCGCTTACTTTTGGCATCTTGTATT 60
Db |||||
64252 ATGTAAACCGAATTTATGGCGCATTTCTTGTGCGCTTACTTTTGGCATCTTGTATT 64193
QY 61 GGCGCAATTTGGCGTGCAGCTTGTGCAATCAACGCCGACCGGTACCCGTCAC 120
Db |||||
64192 GGCGCAATTTGGCGTGCAGCTTGTGCAATCAACGCCGACCGGTACCCGTCAC 64133
QY 121 TTCAAGTCTAAGGAGTTCCCACTCGGCCCTTCTATAGAACCAACCGCG 180
Db |||||
64132 TTCAAGTCTAAGGAGTTCCCACTCGGCCCTTCTATAGAACCAACCGCG 64073
QY 181 GTGCGCTCAACCGGCGCTTGGCGCAATTCGCGCTGTTGAGCGGATTTTGGCA 240
Db |||||
64072 GT-----CAACCGGCGCGCTGCGTGGCGCAATTCGCGCTGTTGAGCGGATTTTGGCA 64019
QY 241 ACTTCTGATAGTTGGCAATGATTTTCAAAATAGCAAAACAGCAGAGAAAGCTGCG 300
Db |||||
64018 TCCTATTAACAGAGCGTACGAAATTTCCGACAGCATCAGGAGAGGATCTGCGCG 63959
QY 301 TTTAAGAGAGTGTGTTCTGTTTATACGTTTCAAAAGATTAACCTTCAGTGGCTT 360
Db |||||
63958 CTAAAGAGAGGATATCTGTTTATAGCGGTGCTGAAAGAACAGGCTGACAACTT 63899
QY 361 AAGGATAAATTCATCAACGCAATCTTAATGTAGAAATTAGGACATCAGAAATGAAAT 420
Db |||||
63898 AAAAAAATCAACGCAATCTTAATGTAGAAATTAGGACATCAGAAATGAAATGAA 63839
QY 421 AAAAAATGTTGATGATTTGGATGCGGTTATGATATATATAAAAAACGGAACA --- 477
Db |||||
63838 GAAAAATATCAATATCAATTTGTCGCGGCTATGTTTACCGGCGGAGGAAAG 63779
QY 478 ---GATGAAATTCAGTGACTTCAATTCGACGAGCTTTTCTATTCGTTTGGTACGAC 534
Db |||||
63778 GATAATGAAAAAGAAAGACTTCTGATGTAAGAGTGTGTTAACCCGATTTAGTTATGAC 63719
QY 535 GGTTTGTATATTTATTCGAGAACATCTTCCCAATCTTTACCGAGCGGGAACCGGTG 594
Db |||||
63718 GGTTTGTATATTTATTCGAGAACCTTCTTCCCAATCTTTACCGAGCGGGAACCGGTG 63659
QY 595 CAATATTCGTTAATTCGAGAACATATGACCGGATGCGCATCGTATCGAAACAGCA 654
Db |||||
63658 CAATATTCGTTAATTCGAGAACATATGACCGGATGCGCATCGTATCGAAACAGCA 63600
QY 655 GGAGATCTTAGCGAAGATTTGGTATCTGTTTATTCGTTTATTCGTTTATTCGAGCAACT 714
Db |||||
63599 --GGTTTCAGTACGAGTTGGGTTATACCAATATTTATGTTATGTTATGTTATGTTGGA 63542
QY 715 TCTTATGCTCGACTCCCGACCGAGCGGAGGAAAAACATCTCTCCCAATATACGGTTGAT 774

QY 1783 CGGATATAAAGCGGCAAAACGAGAAATTTGACGTTGATTTCCGGGAGAAATCGATTCC 1842
DB 97717 CGGGATAAAGAGCGGCAAAACGAGTAATTTACCGTTGATTTCCGGCAAGAAATCGAATTTCC 97658
QY 1843 GGAACGCTGACGGAGAAACCGGTGTACAACTGCTTTCCATATTGAAACCGCGTGATT 1902
DB 97657 GGAACGCTGACGGAGAAACCGGTGTAGAACTGCTTTCCATATTGAAACCGCAAGATT 97598
QY 1903 GAGGCAATGTTTCCACGCGACAGCGGCACTCGGGATACGGCATCAATCTTTCGGGA 1962
DB 97597 GAGGCAATGTTTCTACGCGACAGCGGCACTCGGGAGAACGGCATCAATCTTTCGGGA 97538
QY 1963 AATGATTCGACTAATCTCCAGTTTCAAGCCAAATAATCTTCTTGTAAACGGCGCTTT 2022
DB 97537 AATGTTGACCGACCCCAAACTTCCAGCTAGTAATCTTCCATTAATGATGGGAAATCTCTT 97478
QY 2023 TACGCGCCGACGGCGAGGAATGGCGGTACTATTTTCAATAATGATGGGAAATCTCTT 2082
DB 97477 TACGCGCCGACGGCGAGGAATGGCGGTACTATTTTCAATAATGATGGGAAATCTCTT 97418
QY 2083 GGTATACTGAAGTACTGAAA-----TGAAGCTGAAGCTGAAGTTGAAATGAAGCT 2136
DB 97417 GGTATACTGAAGTACTGAAAATAAAGTTGATTTGAAGCTGAAGTTGATGCTGAAGTT 97356
QY 2137 GGTGTTGGGAAACAGTTAAACCTGAAGCTAAACCCCAATTCGGGTGTTATTCGGTGCG 2196
DB 97357 GATGTTGGCAACAGTTAGAACTGAAGTTAAACCAATTCGGGTGTTATTCGGTGCG 97298
QY 2197 AAGAAAGATAATAAGAGGTTGAAAAATGA 2226
DB 97297 AAGAAAGATATGAGGAGTTGAAAAATGA 97268

RESULT 7
AA23322
ID AA23322 standard; cdna; 2262 BP.
XX
AC AA23322;
DT 11-JUN-1999 (first entry)
XX
DE N. meningitidis strain M990 LbpB cdna.
KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
KW meningitis; diagnosis; treatment; ds.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT 1. .2262
FT /*tag= a
FT /product= "LbpB"
XX
PN W0909176-A1.
XX
XX 25-FEB-1999.
XX
PF 10-AUG-1998; 98WO-EP005117.
XX
XX 15-AUG-1997; 97GB-00017423.
PR 05-FEB-1998; 98GB-00002544.
XX
XX (UYUT-) RIJKSUNIV UTRECHT.
PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
XX
PI Pettersson-Fernholm AM, Tommassen JPM;
XX
XX WPI; 1999-190165/16.
DR
DR P-PSDB; AAW93495.
XX
XX New lactoferrin-binding protein B polynucleotides - obtained from
PT Neisseria meningitidis, used to develop products for the diagnosis,
PT prevention and treatment of neisserial disease, e.g. meningitis.

XX
PS
XX
CC This invention describes novel lactoferrin-binding protein B (LbpB)
CC strains of Neisseria meningitidis. The products of this invention can be
CC used for vaccinating humans against neisserial disease e.g. meningitis.
CC Antibodies raised against the proteins of the invention can be used for
CC diagnosing or treating neisserial disease in humans. The LbpB
CC polypeptides can also be used for identifying compounds which inhibit the
CC polypeptides
XX
SQ Sequence 2262 BP; 698 A; 487 C; 590 G; 487 T; 0 U; 0 Other;
Query Match 64.8%; Score 1442.2; DB 2; Length 2262;
Best Local Similarity 80.3%; Pred. No. 0;
Matches 1828; Conservative 0; Mismatches 383; Indels 66; Gaps 9;
QY 1 ATGTGTAACCGAAATATGCGGCAATGCTGTTGTCCTTACTTTTGGCATCTTTGTATT 60
DB 1 ATGTGTAACCGAAATATGCGGCAATGCTGTTGTCCTTACTTTTGGCATCTTTGTATT 60
QY 61 GCGCGCAATTTGCGGTCGAGCTGCTGTCGAATCAACGCGACCGCG----- 108
DB 61 GCGCGCAATTTGCGGTCGAGCTGCTGTCGAATCAACGCGACCGCGCAACTCTGTCA 120
QY 109 TACCCCGTCACCTTCAAGTCTAAGGACGTTCCCACTCCGCCCCCTGCCAAACCTTCTATA 168
DB 121 GATTCCAATCTTCCAATCTCGGATAAGCTGCTCCAGCTCTCTGCCGAGCTTCGGTA 180
QY 169 GAAACACGCGGTCGCGTCAACCGGCGCTGCGTGGTGGGCAATGCGGCTGTTGAGG 228
DB 181 GAAATCAGCGCGT-----CAAAGCGCGCGCGTGGTGGGCAATGCGGTCGCAAGG 234
QY 229 CGGATTTTCGCAACTTCTGATGAAGTTGCGAATGATTTTCCAAATAGCAAAACAGCAGAA 288
DB 235 CGGAATATCGCAACTTTGATGAATAAATGTAATGAATTTCCCAATAGTANGCAGCGCAG 294
QY 289 GAAAAGCTGCTCGTTTAAAGAGGATGATGTTCTGTTTTTATACGGTTTCAAAAAAGATAA 348
DB 295 GAGTATCTGCGCTCAAGAGAGGATATCTGTTTTTATAGCGGTACCGGAAAGAACAG 354
QY 349 CTTGAGTGGCTTAAGGATAAATTCATCAACGCAATCTTAATGTAGAAATTAGGACATCA 408
DB 355 GCTGCAAACTTTAAAAAGGAAATCAACGAGCGCATCTTAATGCAACCAATCTACAGTCC 414
QY 409 GAAATGAAATAAATAATATGTTATGATGATGTTGATGATGATGATGATGATGATGAT 468
DB 415 GATTTAAAGATGATGCGTATCAATATAAATATGTCGGGCGCGATGATGTTATATAGTA 474
QY 469 AACGGAACAGATGAAATTCAGTGGACTTCAAAATCGCAAGCAGTTTTTCTAATCGTTTGGC 528
DB 475 TATGGAACAGATGAAATCGAACAGAACTCAGCGGTTAAGCGGTTACCCACCGCTTAGGT 534
QY 529 TACGAGGTTTGTATATTTATTCGCGAGAACTCTTCCCAATCTTACCGAGCGGGA 588
DB 535 TATGAGGTTTGTATATTTATTCGCGAGAACTCTTCCCAATCTTACCGAGTGGGGA 594
QY 589 ACGGTCAATATTCGCGTAATCGCAATATATGACCGATGCCATAGTCTATCGAACAGGA 648
DB 595 ACGGTGAATATTCGCGTAATCGCAATATATGACCGATGCCATAGTCTATCGAACAGGT 654
QY 649 AAAGCAGGAGATCTTAGCGAAGATTTGGGTTATCTCGTTTATTACCGTCAAAATGCGGA 708
DB 655 CAGGC--GTTGGCATTGACAATTTGGGTTATATCACATTTTATGTTAAGCATGTTGTT 711
QY 709 GCAACTTCTATGCTCGACTCCGACGCGGAGGAAACATCTCTCCGATATACG 768
DB 712 GCAACTTCTATGCTCGACTCCGACGCGGAGGAAACATCTCTCCGATATACG 771
QY 769 GTTGATTTTCGATAAGAAATCTTTGACGGGTCAATTAATTAATAATCAGTATGTGCAAAAG 828
DB 772 GTTGATTTTCGATAAGAAATCTTTGACGGGTCAATTAATTAATAATCAGTATGTGCAAAAT 831

Claim 2; Page 98-102; 116pp; English.

[illegible]

Db 2032 AAAGCCAGTAATCTTCTCTAGAGGAGGATTTATGTTCCGACGGCGCAGAGTTGGGT 2091
QY 2050 GGTACTATTTCATAATGATGGGAAA 2076
XX ||||| ||||| ||||| |||||
Db 2092 GGTATATATTCAGACAGTACCGGAAA 2118

RESULT 9

AAA81482/c

ID AA81482 standard; DNA; 14652 BP.

XX

AC

XX

XX

DT 04-DEC-2000 (first entry)

XX

DE

XX

N. meningitidis partial DNA sequence gnm_30 SEQ ID NO:30.

XX

Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;

KW antigen; vaccine; diagnosis; infection; antibacterial; identification;

KW Meningococcus B; MenB; ds.

XX

XX

Neisseria meningitidis.

OS

XX

WO200022430-A2.

XX

PN

XX

20-APR-2000.

XX

PF 08-OCT-1999; 99WO-US023573.

XX

PR 09-OCT-1998; 98US-0103794P.

XX

PR 30-APR-1999; 99US-0132068P.

XX

XX

(CHIR) CHIRON CORP.

PA

XX

PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;

XX

PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;

XX

PI Rappuoli R, Pizza M;

XX

XX

WPI; 2000-318079/27.

XX

XX

Isolated nucleotide sequences of Neisseria meningitidis which can be used

PT in the diagnosis and treatment of N. meningitidis infection and other

PT Neisserial infections, for example, N.gonorrhoea.

XX

XX

Claim 7; Page 582-586; 1760pp; English.

PS

XX

The present invention describes methods of obtaining immunogenic proteins

CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent

CC specifically claimed Neisseria meningitidis genomic DNA sequences;

CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA

CC sequences and their corresponding proteins; AAA81254 to AAA81259 and

CC AAA81304 to AAA81321 represent PCR primers used in the isolation of

CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent

CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all

CC used in the exemplification of the present invention. The nucleic acid

CC sequences, protein sequences, and antibodies against them, can be used in

CC the manufacture of a composition. The composition can be used as a

CC medicament (or in the manufacture of a medicament) for treating,

CC preventing or diagnosing infection due to Neisserial bacteria. For

CC example, some of the identified proteins could be components of vaccines

CC against Meningococcus B; against all serotypes, and/or against all

CC pathogenic Neisseriae. Identification of sequences from the bacterium

CC will also facilitate production of biological probes, particularly

CC organism-specific probes. Attempts to make efficacious Meningococcus B

CC vaccines have failed mainly due to antigen tolerance. Multivalent

CC vaccines have also been tried but none have successfully overcome

CC antigenic variability. The provision of further, complete sequences may

CC provide an opportunity to identify secreted or surface exposed proteins

CC that may be presumed targets for the immune system and which are not

CC antigenically variable or at least more conserved than other more

CC variable regions

XX

SQ Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;

Query Match 48.4%; Score 1077.6; DB 3; Length 14652;
Best Local Similarity 84.1%; Pred. No. 1.5e-260;
Matches 1292; Conservative 0; Mismatches 199; Indels 45; Gaps 5;

QY 709 GCAACTTCTTATGTCGCACTGCCGACGACCGGGGAGGAAAACATCTCTGCGGAATATACG 768
Db 14652 GCAACTTCTTATGAGGCTAGGATGCCGACGACGAGGAGAAACATCTCTGCGGAATATACG 14593
QY 769 GTTGATTTTCGATAAGAAAACCTTTGACGGCTCAATTAATTAATAATCAGTATGTGCAAAAG 828
Db 14592 GTTGATTTTCGATAAGAAAACCTTTGATGCGAAGCTGATTAATAATCAGTATGTGCAAAAT 14533
QY 829 AAAACCGATGAA-----AAGAAACCACTGACCACTTTACGACATTTACCGCAACATTTG 879
Db 14532 AAAAGTATCCAAATGAGCCCCAAAACCGCTGACCACTTTACGACATTTACCGCAACATTTG 14473
QY 880 GACGCAACCGCTTTACCGGAGTCCCAAGGTTAAACCGAGTTGAAGACGAGCCACGCT 939
Db 14472 GACGCAACCGCTTTTACCGGAGTCCCAAGGTTAGCACCGAGGTGAAGACGACACACGCT 14413
QY 940 GATAAAGAGCATTTGTTTTTCCATACCGATCCGATCAGCGGCTTTGAGGGCGGTTTTTTC 999
Db 14412 GATAAAGATATTTGTTTTTCCATACCGATCCGATCAGCGGCTTTGAGGGCGGTTTTTTC 14353
QY 1000 GGCATAGGGGGAAGAGCTTCCCGACGGTTTTATCAGCAACGACAAACAGCGTATTCGGC 1059
Db 14352 GGCATAGCGAGAGAGCTTTCGCGACGGTTTTATCAGCAACGACAAACAGCGTATTCGGC 14293
QY 1060 GTATTCCGAGCA---AAAAAACAACGCATCAACCGCAGCAGATACAAATCTCTGCTATG 1116
Db 14292 GTATTCCGAGCAACAAAAACAAGACAGCAAAAAACGACAGATACAAAACTCTGCCCTG 14233
QY 1117 CCGTCTGAAAAACACACCAAAATCTTGATTTCTGAAAAATTTCCGTTGACGAGCGCAGC 1176
Db 14232 TCCTCTGAAAAACAACCAAAATCTTGATTTCTGAAAAATTTCCGTTGACGAGCAAGT 14173
QY 1177 GATAAAATGCCCGCCCGCTTTGCCATTTCCCGCTCTGCCGATTTTGGCCATCTCCGACAAA 1236
Db 14172 GATAAAATCCCCGTGAGTTTGCCATTTCTCTATGCCGATTTTGGTCATCCCGACAAA 14113
QY 1237 CTCTCTGTCGAGGGCGTGAATTCCTTTGGTTAGCAAGAGAAAACCATCGAGCTTGCC 1296
Db 14112 CTCTCTGTCGAGGGCGTGAATTCCTTTGGTTAGCAAGAGAAAACCATCGAGCTTGCC 14053
QY 1297 GACGCGAGGAAATGACCGCTCCGCTGTTGTTGGCATTTTCTGACCTATGTGAAACTCGGA 1356
Db 14052 GATGTTAGGAAACGACAAATCCGNAACCTGCTGCGATTTTCTGACCTATGTGAAATCGGA 13993
QY 1357 CGGATAAAATCTGACCCGCCCAAGTAACCAAGCGGAGAGATAAAGGGAGAGATGAA 1416
Db 13992 CGGATGCAAAACCGAAACGTCGCCGCCCAACCGAAGCGGACGAGGAGAGGAGCGAA 13933
QY 1417 GAGGATACAGCGCTTGTGTAACGACGAGAGGACGGAAGTGAAGCGCGCAGAGGCGAGC 1476
Db 13932 GAGGATACAGCGCTTGTGTAACGAGAGGCGGAGACGAAATTCGACGATGAA----- 13879
QY 1477 GAAGGAGCGCAAGACGAAATTCGGCGATGAAGGAGAGGTTGCGGAAGACGAGCGCAGAA 1536
Db 13878 GAAGGACCCGAGACGCGCGCTTAAGACGAGGAGCGGAGAGGAGAGGAGCGGTAGAA 13819
QY 1537 AACGAAGGCGCGGAGAGAGACGAAAGCTGAAGAACCTCGAAGAACCCGGAAGAGATCCCG 1596
Db 13818 GGTGAA-----GATGAAGCTGAAGAACCCGGAAGAGATCCCG 13780
QY 1597 GCGAAGGCGCGGTGTTGTTGACGCGCATCTGCGCCCTCGGAGCTCTTAAAGGC 1656
Db 13779 ACGAAGAGGCGGACGCGGTTTCAGACGGCATCTCTGCCGCTCGGAGGCGCCCTTAAAGGC 13720
QY 1657 AGCGATATCCACCTTTTCTTGAAGGTTATCCGACGCGGAGGCGGATATTCGCAAACT 1716
Db 13719 AGGAACATCGACCTTTTCTTGAAGGTTATCCGACGCGGAGGAGATATTCGCAAACT 13660

Db 652 GTTATACCATATTTATGTAATGTAATGGGCAACTCTTATGAGCTA 702

RESULT 13

ABS67377

ID ABS67377 standard; DNA; 3300 BP.

XX XX

AC ABS67377;

XX XX

DT 29-NOV-2002 (first entry)

XX XX

DE Neisseria gonorrhoeae lbpA gene.

XX XX

KW Gram-negative bacterial bleb; PorB; outer membrane protein;

KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;

KW protective antigen; antibacterial; vaccine; gene; ds.

XX XX

OS Neisseria gonorrhoeae.

XX XX

PN WO200262380-A2.

XX XX

PD 15-AUG-2002.

XX XX

PF 08-FEB-2002; 2002WO-EP001356.

XX XX

PR 08-FEB-2001; 2001GB-00003169.

XX XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX XX

PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;

XX XX

DR WPI; 2002-657510/70.

XX XX

DR P-PSDB; ABG31056.

XX XX

PT Novel gram-negative bacterial bleb presenting on its surface PorB outer

PT membrane protein from Chlamydia trachomatis or protective antigen from

PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.

XX XX

PS Disclosure; Page 48-49; 75pp; English.

XX XX

CC The present invention relates to a new gram-negative bacterial bleb

CC presenting on its surface the PorB outer membrane protein from Chlamydia

CC trachomatis, or a protective antigen from C. pneumoniae. The invention is

CC useful for preventing C. trachomatis or C. pneumoniae infection in a

CC host. The present nucleic acid sequence represents a Neisseria

CC gonorrhoeae gene as described in the invention

XX XX

SQ Sequence 3300 BP; 897 A; 807 C; 921 G; 675 T; 0 U; 0 Other;

XX XX

Query Match 10.8%; Score 239.8; DB 6; Length 3300;

Best Local Similarity 91.8%; Pred. No. 1.1e-49;

Matches 269; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

1934 CTCGGGTAACGGCATCAATCTTCGGGAATGATTCGACTAATCTCCAGTTTCAAG 1993

Db 1 CTCGGTAACGGCATCAATCTTCGGGAATGATTCGACTAATCTCCAGTTTCAAG 60

XX XX

1994 CCAATAATCTTCTTTAAACAGCGGCTTTTACGGCCGCGAGGAGGATGGCGGTA 2053

XX XX

61 CCGACATCTTCTTTAAACAGCGGCTTTTACGGCCGCGAGGAGGATGGCGGCA 120

XX XX

2054 CTATTTTCAATAATGATGGGAATCTCTTGTTGTAATCTGAAGATCTGAAGATCTG 2113

Db 121 CTATTTTCAATAATGATGGGAATCTCTTGTTGTAATCTGAAGATCTGAAGATCTG 172

XX XX

2114 AAGCTGAAGTTGAAATGAAGCTGGTGTTCGGCAACAGTTAAACCTGAAGCTTAAACCCC 2173

XX XX

173 ----TGAAGTTGAAATGAAGCTGATGTTGGCAACAGTTAGAACCTTGAAGTTAAACCCC 228

XX XX

2174 AATTCCGGCGTGGTATTCGGTTCGGAAGAAAGATAATAAGAGGTGCGAAATGA 2226

XX XX

229 AATTCCGGCGTGGTATTCGGTTCGGAAGAAAGATAATAAGAGGTGCGAAATGA 281

RESULT 14

AAS90909

ID AAS90909 standard; cDNA; 379 BP.

XX XX

AC AAS90909;

XX XX

DT 13-FEB-2002 (first entry)

XX XX

DE DNA encoding novel human diagnostic protein #26713.

XX XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX XX

OS Homo sapiens.

XX XX

PN WO200175067-A2.

XX XX

PD 11-OCT-2001.

XX XX

PF 30-MAR-2001; 2001WO-US008631.

XX XX

PR 31-MAR-2000; 2000US-00540217.

XX XX

PR 23-AUG-2000; 2000US-00849167.

XX XX

PA (HYSE-) HYSEQ INC.

XX XX

PI Drmanac RT, Liu C, Tang YT;

XX XX

DR WPI; 2001-639362/73.

XX XX

DR P-PSDB; ABG26722.

XX XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX XX

PS Claim 1; SEQ ID NO 26713; 103pp; English.

XX XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic

CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX XX

SQ Sequence 379 BP; 207 A; 25 C; 118 G; 29 T; 0 U; 0 Other;

XX XX

Query Match 4.1%; Score 91.2; DB 5; Length 379;

Best Local Similarity 59.8%; Pred. No. 1.1e-12;

Matches 153; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

1348 AAATCTCGACGGTAAATAAACTGACCGCCGACCAAGTAACCAAGCGGAGATAAAGGG 1407

Db 105 AAACAAAACAAAGACAGAGATATAAGAGAGAGAGAGAGAGAGAGAGAGAGAA 164

XX XX

1408 AAGGTGAAGAGGATACAGCGCTTGGTTAAGCAGAAAGAGGACCGAAGATGAAGCGCA 1467

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 12:38:10 ; Search time 161.734 Seconds
(without alignments)
7637.968 Million cell updates/sec

Title: US-10-735-098-5
Perfect score: 2226
Sequence: 1 agtgttaacgaattatgg.....ataaagaggtggaaaaatga 2226

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A-COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B-COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A-COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B-COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTCUS-COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
C 1	89	4.0	7218	1	US-08-232-463-14
C 2	75	3.4	929	4	US-09-671-317-14
C 3	75	3.4	1001	4	US-09-671-317-439
C 4	72.6	3.3	2230	3	US-08-448-194-7
5	72.6	3.3	2230	3	US-08-867-921-7
6	72.2	3.2	43795	3	US-08-742-185-101
C 7	69.8	3.1	16442	3	US-08-781-891-208
C 8	69.8	3.1	16442	3	US-09-618-166-208
9	68.2	3.1	1276	3	US-09-177-325-2
10	68.2	3.1	1276	3	US-09-411-812A-2
11	68.2	3.1	1276	4	US-09-590-113-2
12	66.8	3.0	390	3	US-09-197-649-7
13	65	2.9	3211	2	US-08-574-959A-8
14	65	2.9	3211	3	US-09-357-014-8
15	65	2.9	3901	2	US-08-574-959A-6
16	65	2.9	3901	3	US-09-357-014-6
17	64.6	2.9	3489	3	US-08-728-323A-1
18	64.6	2.9	3489	4	US-09-298-568-1
19	64.6	2.9	3489	4	US-09-410-399-1
C 20	64.6	2.9	32207	2	US-08-770-379-20
C 21	64.6	2.9	32207	3	US-08-757-669A-20
C 22	64.6	2.9	32207	4	US-09-230-371A-20
C 23	64	2.9	51259	3	US-08-781-891-209
C 24	64	2.9	51259	4	US-09-618-166-209
25	63.6	2.9	2139	4	US-09-059-584-50
26	62.6	2.8	2696	1	US-07-961-522-1
27	62.6	2.8	2696	1	US-08-217-438-1

28	62.6	2.8	2696	1	US-08-321-978-1
29	62.6	2.8	2696	2	US-08-710-584-1
30	60.4	2.7	478	4	US-09-621-976-10407
31	60.4	2.7	1280	4	US-09-220-132-155
C 32	60.4	2.7	1926	4	US-09-249-585A-4
C 33	60.4	2.7	1931	2	US-09-130-114-2
34	59.6	2.7	125157	4	US-09-913-514-2
35	58.8	2.6	696	3	US-09-461-697-193
36	58.8	2.6	699	3	US-09-461-697-191
37	58.8	2.6	717	3	US-09-461-697-189
38	58.8	2.6	774	3	US-09-461-697-187
39	58.8	2.6	819	3	US-09-461-697-185
40	58.8	2.6	1869	4	US-09-461-697-184
41	58	2.6	1926	4	US-09-249-585A-2
42	58	2.6	1926	4	US-09-410-399-3
43	58	2.6	2580	3	US-09-050-863-2
44	58	2.6	2580	4	US-09-359-081-2
C 45	58	2.6	5452	2	US-09-130-114-1

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/POCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
Query Match 4.0%; Score 89; DB 1; Length 7218;

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Best Local Similarity 3.8%; Pred. No. 1.5e-13;
Matches 14; Conservative 242; Mismatches 117; Indels 0; Gaps 0;

QY 1274 AAGAGAAACCATCGAGCTTCCGACGGCAGGAAATGACCGTCGCTGTTGTCGATT 1333
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1414 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1355
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1334 TTCTGACCTATGTGAACCTCGACGATAAACCTGACGCCACCAATACCAAGG 1393
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1354 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1295
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1394 CGGAGATAGAGGAGATGAAGGATACAGGCTTGGTAAACGAGGAGGACCG 1453
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1294 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1235
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1454 AAGATGAAGCCGACGAGGACGAGGAGGCGAAGCAAAATCGCGATGAAGGAGG 1513
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1234 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1514 GTGCGGAGAGCAAGCCGACGAGGAGGAGGCGGAGGAGGAGGAGGAGGAGG 1573
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1174 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1115
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1574 AAGAACCCGAGAGAAATCGCGGACGAGGCGGCGGTGTTGTTGATCGACGCTCC 1633
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1114 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1055
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1634 CCGCTCCGAGC 1646
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1054 CTCGACCTGCAGC 1042
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 2
US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-363 : polymorphic base A or G
; NAME/KEY: misc.binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-363.misl, potential
; NAME/KEY: misc.binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-454-363.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 139..158
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind

```

```

; LOCATION: 634..652
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc.binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-454-363 potential probe
; NAME/KEY: misc.feature
; LOCATION: 674..679,881..882,892..893
; OTHER INFORMATION: n=a, g, c or t
US-09-671-317-14

Query Match 3.4%; Score 75; DB 4; Length 929;
Best Local Similarity 59.7%; Pred. No. 2.8e-10;
Matches 138; Conservative 0; Mismatches 91; Indels 2; Gaps 1;

QY 1397 AAGATAAGGAGGATGAAGGATACAGGCTTGGTAAACGACGAGGAGGAGGAGG 1456
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 872 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 813
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1457 ATGAAGCCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1516
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 812 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 753
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1517 CGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1576
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 752 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 695
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1577 AACCCGAGAGAGATCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1627
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 694 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 644
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 3
US-09-671-317-439/c
; Sequence 439, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 439
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-242 : deletion AT
; NAME/KEY: misc.binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-242.misl, potential
; NAME/KEY: primer_bind
; LOCATION: 260..279
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 755..773
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc.feature
; LOCATION: 795..800

```



```
; APPLICANT: Sakin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins, And
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: LUD 5525
; CURRENT APPLICATION NUMBER: US/09/177,325B
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 2
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-177-325-2

Query Match
Best Local Similarity 3.1%; Score 68.2; DB 3; Length 1276;
Matches 124; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1386 ACCAAAGCGGGAAGATTAAGGGAAGGATGAAGAGGATCAAGGCTTGGTTAAGCAAGCAAGA 1445
Db 713 AGCAGCAGCAGAGTAATAGTAGTAGAAGCAGGAAGAGGAGGAAGAGGAGGAGGAGGA 772
QY 1446 AGGCACCGGAAGATGAAGCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1505
Db 773 GGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 832
QY 1506 AGGAGGAGGTGCGGAAGACGAAAGCCGCAAGAAACGAAAGCGGCGGAGGAGGAGGAGGAGGAG 1565
Db 833 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 892
QY 1566 AGAAGCTGAAGAACCCGGAAGAGAGATCGCGGCAGAA 1602
Db 893 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 929

RESULT 10
US-09-411-812A-2
; Sequence 2, Application US/09411812A
; Patent No. 6261778
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins, And
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: LUD 5525.1 CIP
; CURRENT APPLICATION NUMBER: US/09/411,812A
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 09/177,325
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-411-812A-2

Query Match
Best Local Similarity 3.1%; Score 68.2; DB 3; Length 1276;
Matches 124; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1386 ACCAAAGCGGGAAGATTAAGGGAAGGATGAAGAGGATCAAGGCTTGGTTAAGCAAGCAAGA 1445
Db 713 AGCAGCAGCAGAGTAATAGTAGTAGAAGCAGGAAGAGGAGGAGGAAGAGGAGGAGGAGGAGGA 772
QY 1446 AGGCACCGGAAGATGAAGCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1505
Db 773 GGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 832
QY 1506 AGGAGGAGGTGCGGAAGACGAAAGCCGCAAGAAACGAAAGCGGCGGAGGAGGAGGAGGAGGAG 1565
Db 833 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 892
```

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QY 1566 AGAAGCTGAAGAACCCGGAAGAGAGATCGCGGCAGAA 1602
Db 893 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 929

RESULT 11
US-09-590-113-2
; Sequence 2, Application US/09590113
; Patent No. 6306389
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sakin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins, And
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: LUD 5525
; CURRENT APPLICATION NUMBER: US/09/590,113
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/177,325
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 2
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-590-113-2

Query Match
Best Local Similarity 3.1%; Score 68.2; DB 4; Length 1276;
Matches 124; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1386 ACCAAAGCGGGAAGATTAAGGGAAGGATGAAGAGGATCAAGGCTTGGTTAAGCAAGCAAGA 1445
Db 713 AGCAGCAGCAGAGTAATAGTAGTAGAAGCAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 772
QY 1446 AGGCACCGGAAGATGAAGCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1505
Db 773 GGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 832
QY 1506 AGGAGGAGGTGCGGAAGACGAAAGCCGCAAGAAACGAAAGCGGCGGAGGAGGAGGAGGAGGAG 1565
Db 833 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 892
QY 1566 AGAAGCTGAAGAACCCGGAAGAGAGATCGCGGCAGAA 1602
Db 893 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 929

RESULT 12
US-09-197-649-7
; Sequence 7, Application US/09197649
; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk, Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/C1-CON
; CURRENT APPLICATION NUMBER: US/09/197,649
; CURRENT FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: 07/829,461
; EARLIER FILING DATE: 1992-01-31
; EARLIER APPLICATION NUMBER: 07/739,055
; EARLIER FILING DATE: 1991-08-01
; EARLIER APPLICATION NUMBER: 07/561,968
; EARLIER FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match 3.0%; Score 66.8; DB 3; Length 390;
Best Local Similarity 55.0%; Pred. No. 2.8e-08;
Matches 131; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
QY 1391 AGCGCGAAGATAAAGGGAAGGATGAAGAGATACAGGCGTTGTAAACGACGAAGAGCA 1450
Db 136 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 195
QY 1451 CGGAGATGAAGCGGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1510
Db 196 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 255
QY 1511 GAGGTGCGGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1570
Db 256 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 315
QY 1571 CTGAGAACCCGAGAGAAATCGCGGAGAGGCGGCGGTGTTGTTTCAGACGGCAT 1628
Db 316 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 373

RESULT 13

US-08-574-959A-8
Sequence 8, Application US/08574959A
Patent No. 5952224
GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 439..3157
US-08-574-959A-8

Query Match 2.9%; Score 65; DB 2; Length 3211;
Best Local Similarity 53.8%; Pred. No. 2.8e-07;
Matches 134; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
QY 1376 CAGCAAGTAAACCAAGGCGGAAGATAAAGGAAGATGAAGAGGATGAAGAGGATGAAGAGG 1435
Db 2372 CAGTTATTATATCAACAGCAGTCAGTATGAAGAGGAGGAGGAAGAGGAGGAAGAAG 2431
QY 1436 ACGACGAAGAAGCGCAGGAAGATGAAGCGCGCAGAGGCGAGGAGGAGGAGGAGGAGGAG 1495
Db 2432 AAGAAGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2491
QY 1496 TCGGCGATGAAGAGGAGGAGTGGGAAGACGAAAGCCGCAAAACGAAAGCGCGCGAGAG 1555
Db 2492 TTGAGGAAGAGGAGGAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2551
QY 1556 ACGAGCTGAAGAACCTGAGAACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1615
Db 2552 AGTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2611
QY 1616 GTTCAGACG 1624
Db 2612 ATGAGGAGG 2620

RESULT 14

US-09-357-014-8
Sequence 8, Application US/09357014
Patent No. 6291645
GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 439..3157
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-357-014-8

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 11:49:00 ; Search time 5079.42 Seconds
(without alignments)
13086.780 Million cell updates/sec

Title: US-10-735-098-5

Perfect score: 2226

Sequence: 1 atgtgttaaacgaattatgg.....ataagaggtggaataatga 2226

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_est3.*
12: gb_est4.*
13: gb_est5.*
14: gb_estfun.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.4	4.4	395	29	CE760553
C 2	92.4	4.2	434	14	CA745444
3	92.4	4.2	980	13	BU944408
C 4	91.8	4.1	263	13	BU005139

5	91.8	4.1	665	13	BU432980
6	91.8	4.1	1096	14	CK206118
C 7	91.6	4.1	960	28	CC143364
8	91.4	4.1	341	29	CE510654
9	91	4.1	264	13	BQ241566
C 10	90.2	4.1	691	28	BH040136
11	89.8	4.0	358	28	AZ582992
12	89.8	4.0	617	28	AZ296172
C 13	89.4	4.0	232	29	CG321416
C 14	89.4	4.0	605	28	BZ222147
C 15	89.2	4.0	311	14	CA699402
C 16	89.2	4.0	617	14	CA743799
C 17	89	4.0	697	28	AZ374916
18	88.4	4.0	575	10	BF707975
C 19	88.4	4.0	739	28	BZ220379
C 20	88.4	4.0	879	28	AZ550718
21	88.4	4.0	942	28	BH148582
C 22	88.4	4.0	3743	11	AK048184
C 23	88.2	4.0	265	14	CA607797
24	88.2	4.0	540	28	AZ813205
25	88.2	4.0	634	28	AZ008814
26	88	4.0	332	14	CA566759
27	87.8	3.9	278	13	BQ460618
28	87.6	3.9	477	14	CD311846
29	87.6	3.9	531	14	CD915362
30	87.6	3.9	571	28	AZ952930
31	87.4	3.9	633	28	AZ855793
32	87	3.9	447	9	AA110445
33	87	3.9	466	28	AZ296286
34	86.8	3.9	799	28	BZ201507
C 35	86.8	3.9	880	28	AZ529191
36	86.6	3.9	223	13	CA022136
C 37	86.6	3.9	289	14	CA716220
C 38	86.6	3.9	906	28	BH153606
39	86.6	3.9	924	13	BQ925195
40	86.4	3.9	293	13	BQ459561
41	86.4	3.9	295	13	BU976670
42	86.4	3.9	340	13	BQ462203
43	86.4	3.9	675	28	BZ104011
44	86.4	3.9	866	28	AZ527885
45	86.4	3.9	890	28	BH146886

ALIGNMENTS

RESULT 1
CE760553

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CE760553 tigr-gss-dog-1700036997532 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE760553
CE760553.1 GI:37101172
GSS
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 395)
Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627

Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org

[illegible]

Query Match 4.2%; Score 92.4; DB 13; Length 980;
 Best Local Similarity 55.9%; Pred. No. 3.3e-07;
 Matches 147; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1385 AACCAAGCGGGAAGATAAGGAAGGATACAGAGGATACAGCGTTGGTAAAGCGAAG 1444
 |||
 Db 483 AAGAGAAG 542
 |||

QY 1445 AAGGCACGGAAGATGAAGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1504
 |||
 Db 543 AAGAAGAAGGAG 602
 |||

QY 1505 AAGGAGGAGTGGGAG 1564
 |||
 Db 603 AAGGAGGAG 662
 |||

QY 1565 AAGAACCTGGAAGAACCCGAGAGAGATCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 1624
 |||
 Db 663 AAGAAGAAG 722
 |||

QY 1625 GCATCTGCTCCCTCGGAGAGCT 1647
 |||
 Db 723 GCCGCTCGGCTCGAGAGCT 745
 |||

RESULT 4
 BU005139/c
 LOCUS QG7D20.YG.abi OG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
 DEFINITION QG7D20, mRNA sequence.
 ACCESSION BU005139
 VERSION BU005139.1 GI:22439534
 KEYWORDS EST.
 SOURCE Lactuca sativa
 ORGANISM Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichoriaceae; Lactuca.
 1 (bases 1 to 263)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
 Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
 Lai, Z., Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://compgenomics.ucdavis.edu/
 Unpublished (2002)
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmudson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
 singleton, see http://cgdb.ucdavis.edu/ for details.
 Plate: QG7 row: D column: 20.

FEATURES

source

1. .263
 Location/Qualifiers
 /organism="Lactuca sativa"
 /mol_type="mRNA"
 /cultivar="L.serriola"
 /db_xref="taxon:4236"
 /clone="QG7D20"
 /lab_host="E.coli"
 /note="Vector: pBRcDNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library

ORIGIN

Query Match 4.1%; Score 91.8; DB 13; Length 263;
 Best Local Similarity 60.7%; Pred. No. 4e-07;
 Matches 150; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1362 AAAAACTGACCCCGCAGCAAGTAAACCAAGCGGAAGATAAAGGAGGATCAAGAGGA 1421
 |||
 Db 262 ACAGACAGAAACAG 203
 |||

QY 1422 TACAGCGCTTGTAAACGACGAAAGGACCGAAGATGAAGCCGAGAGAGCGGAGG 1481
 |||
 Db 202 AGAAGAAG 143
 |||

QY 1482 AGGCCGAGACGAAATCGCGATGAGGAGGAGGTGGGAGAGACGAGCCGCGAAGCGA 1541
 |||
 Db 142 AGAAGAAG 83
 |||

QY 1542 AGGCGCGGAG 1601
 |||
 Db 82 AGACGAG 23
 |||

QY 1602 AGGCGGC 1608
 |||
 Db 22 AGAAGAC 16
 |||

RESULT 5

BU432980

LOCUS

DEFINITION

BU432980 665 bp mRNA linear EST 29-NOV-2002

603221001F1 CSEQRBN10 Gallus gallus cDNA clone ChEST215a2 5', mRNA

sequence.

ACCESSION BU432980

VERSION BU432980.1 GI:25922291

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 665)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

2233534

12445392

COMMENT

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. .665

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="Layer and broiler"

/db_xref="taxon:9031"

/clone="ChEST215a2"

/sex="Male and female"

/tissue_type="Chondrocytes isolated from growth plate

cartilage"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="CSEQRBN10"

/note="Vector: pBluescript II KS(+); Site1: EcoRI;

Site2: NotI; This normalized library was constructed from

1 million independent clones. cDNA synthesis was initiated

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .960
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="liverpool"
/db_xref="taxon:7159"
/clone_lib="Notre Dame Liverpool"
/note="Vector: pBEBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

ORIGIN

Query Match
Best Local Similarity 4.1%; Score 91.6; DB 28; Length 960;
Matches 157; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 1387 CCAAGCGGAGATGAAGGGAAGGATGAAGAGGATACAGCGCTTGTGTAACGACGAAGAA 1446
DB 425 CAAGAAGAAGAAGAAGAAGAAGAAGAAAAAGAGAAGAAGAAGAAGAAGAAGAAGAAGA 484
QY 1447 GGCACGGAGATGACCGCGAGAGGCGACGAAGGCGGAGACGAAATCGCGCGATGAA 1506
DB 485 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 544
QY 1507 GGAGGAGTGGCGAAGACGAGCGCGAGAAACGAAACGAGCGCGAGAGAGCGAGCTGAA 1566
DB 545 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 604
QY 1567 GAACCTGAAGAACCGGAGAGAGATTCGCGCAGAGCGCGCGTGTGTTTCAGACGCG 1626
DB 605 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 664
QY 1627 ATCTGCGCGCTCCGGAGCTCTTAA 1652
DB 665 TTCCCCAACGCGCCTGAAGGTATTAA 690

RESULT 8
CE510654
LOCUS
DEFINITION
tigr-gss-dog-17000327383461 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE510654
VERSION
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 341)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
JOURNAL
MEDLINE
PUBMED
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1. .341
/organism="Canis familiaris"
/mol_type="genomic DNA"

FEATURES
source

ORIGIN

Query Match
Best Local Similarity 4.1%; Score 91.4; DB 29; Length 341;
Matches 143; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1385 AACCAAGCGGAGATGAAGGGAAGGATGAAGAGGATACAGCGCTTGTGTAACGACGAAG 1444
DB 1 AAGAAGAAGAAGAAGAAGAAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
QY 1445 AAGCAGCGGAGATGAAGCGCGAGAGGCGAGCGAGGCGGAGAGCGAGGAGGAGGAGGATG 1504
DB 61 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 120
QY 1505 AAGGAGGAGTGGCGAAGACGAGCGCGAGAAACGAAACGAGCGCGGAGAGGAGGAGGAGCTG 1564
DB 121 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 180
QY 1565 AAGAACTGAAGAACCGGAGAGAGATTCGCGCAGAGAGCGCGCGCTGG 1613
DB 181 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 229

RESULT 9
BQ241566
LOCUS
DEFINITION
TaE05003E07R TaE05 Triticum aestivum cDNA clone TaE05003E07R, mRNA
sequence.
BQ241566
VERSION
KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 264)
Cloutier,S.
Wheat functional genomics - Glenlea developing seeds cDNA libraries
Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Daffoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 003 row: E column: 07
Seq primer: M13 Reverse.
Location/Qualifiers
1. .264
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TaE05003E07R"
/tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="E. coli DH10B"
/clone_lib="TaE05"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
NotI; Site_2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"

FEATURES
source

ORIGIN

Query Match
4.1%; Score 91; DB 13; Length 264;

Best Local Similarity 63.5%; Pred. No. 5.7e-07;
Matches 139; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1385 AACCAAGCGGAGATAAAGGAGGATGAAGAGGATACAGCGTGTGTAACGAGAG 1444
DB 22 AAGAAGAGTGAAG 81
QY 1445 AAGGACCGAGATGAAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1504
DB 82 AAGAAG 141
QY 1505 AAGGAGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1564
DB 142 AAGAAG 201
QY 1565 AAGAAGCTGAAG 1603
DB 202 AAGAAG 240

RESULT 10
BH040136/c
LOCUS
DEFINITION
RPCI-24-255A23.TV RPCI-24 Mus musculus genomic clone
RPCI-24-255A23, genomic survey sequence.
ACCESSION
BH040136
VERSION
BH040136.1 GI:14818806
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 691)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End sequences from Library RPCI-24
TITLE
Unpublished (1999)
JOURNAL
Other_GSSs: RPCI-24-255A23.TV
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
Page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 255 row: A column: 23
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .691
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-255A23"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/notes="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."

ORIGIN

Query Match 4.1%; Score 90.2; DB 28; Length 691;
Best Local Similarity 58.9%; Pred. No. 8.5e-07;

Matches 155; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 1359 GATTAATACTACCCCGCAGCAAGTAACCAAGCGGAGGATGAAGGAGGATGAAGA 1418
DB 510 GAAGAATAAGGAAG 451
QY 1419 GGATACAGCGTGTGTAACGACGAAGAGGACCGCAAGATGAAGCGCAGAGAGCGGAG 1478
DB 450 AGAAG 391
QY 1479 AGGAGCGGAGAGACGAAATCGGCGATGAAGAGGAGAGGTGCGGAGACGAAGCGCGAGAAA 1538
DB 390 AGGAG 331
QY 1539 CGAAGCGGCGGAG 1598
DB 330 AGAAG 271
QY 1599 AGAAGCGGCGGCGTGGTTCAG 1621
DB 270 TGAAG 248

RESULT 11
AZ582992
LOCUS
DEFINITION
1M0376K12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0376K12 R, genomic survey sequence.
ACCESSION
AZ582992
VERSION
AZ582992.1 GI:11702428
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 358)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedermauern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0376 row: K column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 358.

FEATURES
source
1. 358
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0376K12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

```

ORIGIN
Query Match      4.0%; Score 89.4; DB 29; Length 232;
Best Local Similarity 63.0%; Pred. No. 1.1e-06;
Matches 138; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1385 AACCAAGCGCGAAGATAAGGAGGATGAAGAGATACACGGCTGGTAAACGACGAG 1444
Db 226 AAGAAGAGAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
QY 1445 AAGGACGAGAGATGAAGCGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1504
Db 166 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 107
QY 1505 AAGGAGGAGGTCGCGAAGAGAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1564
Db 106 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 47
QY 1565 AAGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1603
Db 46 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8

```

```

RESULT 14
BZ222147/c
LOCUS
DEFINITION
CH230-361K14.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-361K14, genomic survey sequence.

```

```

ACCESSION
BZ222147
VERSION
BZ222147.1 GI:23880505

```

```

KEYWORDS
GSS.
SOURCE
Rattus norvegicus (Norway rat)

```

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ORGANISM
Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

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REFERENCE
1 (bases 1 to 605)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)

```

```

OTHER_GSSs: CH230-361K14.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pjejong@mail.choi.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or_ering_information.htm). BAC end
plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 361 row: K column: 14
Seq primer: T7
Class: BAC ends.

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FEATURES
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/sex="Female"
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/note="Vector: pTARBAC1.3; Site_1: MboI; Site 2: MboI;
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```

Pieter de Jong"

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ORIGIN
Query Match      4.0%; Score 89.4; DB 28; Length 605;
Best Local Similarity 62.1%; Pred. No. 1.2e-06;
Matches 141; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

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Db 584 AGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525
QY 1437 CGACGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1496
Db 524 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 1497 CGGCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1556
Db 464 AGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 1557 CGAAGCTGAAGAACCTGAAGAACCCGGAAGAACCAAGAACCAAGAACCAAGAACCAAGAAC 1603
Db 404 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 358

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RESULT 15
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LOCUS
DEFINITION
wlk8.pk0017.e4 wlk8 Triticum aestivum cDNA clone wlk8.pk0017.e4 5'
end, mRNA sequence.

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ACCESSION
CA699402
VERSION
CA699402.1 GI:25421195

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KEYWORDS
EST.
SOURCE
Triticum aestivum (bread wheat)

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ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

```

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REFERENCE
1 (bases 1 to 311)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
Dupont Wheat cDNA Sequence
Unpublished (2002)

```

```

AUTHORS
Contact: Scott V. Tingey
Crop Genetics
E. I. Dupont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.

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/clone_lib="wlk8"
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ORIGIN
Query Match      4.0%; Score 89.2; DB 14; Length 311;
Best Local Similarity 62.5%; Pred. No. 1.3e-06;
Matches 130; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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Db 216 GAAGATGAAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 157
QY 1456 GATGAAGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1515

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:53:30 ; Search time 8482.05 Seconds
(without alignments)
11558.757 Million cell updates/sec

Title: US-10-735-098-7
Perfect score: 2262
Sequence: 1 atgttaaacccgaattatgg.....tcgagaggtggaaaaaatga 2262

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
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- 18: em.in.*
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- 20: em.om.*
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- 41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2262	100.0	2262	6	AF123381 Neisseria
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C 4	1558	68.9	9955	1	BD074758 Neisseria
C 5	1558	68.9	349980	6	AE002504 Neisseria
6	1465.2	64.8	2277	1	AX044033 Sequence
7	1465.2	64.8	2277	1	AF022781 Neisseria
8	1465.2	64.8	2277	6	A98968 Sequence 1
9	1465.2	64.8	2277	6	BD074755 Neisseria
10	1463.6	64.7	2537	1	AF049349 Neisseria
C 11	1442.6	63.8	326301	1	AF031432 Neisseria
12	1442.2	63.8	2226	1	AF123380
13	1442.2	63.8	2226	6	AF123380 Neisseria
14	1442.2	63.8	2226	6	A98972
15	1433.4	63.4	2519	1	BD074757
16	1291.8	57.1	2124	1	AF123383
17	1291.8	57.1	2124	6	BD072890
18	1291.8	57.1	2124	6	BD074759
19	1250.6	55.3	2169	1	AF123382
20	1250.6	55.3	2169	6	A98970
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24	406.8	18.0	3398	1	NMLBPAG
25	169.2	7.5	3300	1	NGUL16260
26	169.2	7.5	3300	6	AX685922
27	153.4	6.8	3171	1	NM1ROA
C 28	116.8	5.2	110000	2	AC115426_0
C 29	112	5.0	214856	2	AC113738
30	109.6	4.8	233152	2	AC113738 Rattus no
31	107.6	4.8	119191	9	AP004782
C 32	107	4.7	271336	2	AC111017
C 33	106.2	4.7	75588	9	AL356742
C 34	105.8	4.7	142658	2	AC129074
C 35	105.8	4.7	244010	2	AC105848
C 36	105.4	4.7	173737	2	AC120362
37	105.4	4.7	198648	2	AC113517
38	105	4.6	213739	2	AC113937
39	104.6	4.6	233713	2	AC133034
C 40	104.2	4.6	161325	10	AC102576
C 41	104	4.6	213753	2	AC110715
C 42	104	4.6	309266	2	AC106972
C 43	103.8	4.6	224344	10	AL606969
C 44	103.8	4.6	290138	2	AC097202
C 45	103.6	4.6	153771	2	AC101964

ALIGNMENTS

RESULT 1
LOCUS AF123381
DEFINITION Neisseria meningitidis strain m990 lactoferrin-binding protein precursor (lbpB) gene, complete cds.
ACCESSION AF123381
VERSION AF123381.1
KEYWORDS GI:4884688
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 2262)
AUTHORS Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tommassen,J.

Pred. No. is the number of results predicted by chance to have a

Sequence variability of the meningococcal lactoferrin-binding

protein lbpB
Gene 231 (J-2), 105-110 (1999)
MEDLINE 99250255
PUBMED 10231574
REFERENCE 2 (bases 1 to 2262)
AUTHORS Patterssoh, A., van der Biezen, J., Joosten, V., Hendriksen, J., and Tomassen, J.

TITLE Direct Subdivision
JOURNAL Submitted (06-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
FEATURES Location/Qualifiers

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Query Match 100.0%; Score 2262; DB 1; Length 2262;
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QY 1 ATGTGTAACCGAATTATGCGCATTTGCTGTTGGCCCTTACTTTAGCATCTTGATC 60
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DB 61 GCGGCAATTTCGGCGTACAGCCTGTTGTCGAATCAACGCGGCGGCAACTCTGTCA 120
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DB 121 GATTCGAATCTTCCAACTCGGGAAGCCTGCTCCAGCTCTCGCGAGCCTTCGGTA 180
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DB 181 GAAATACGCGGTCGAAGCGGCGCGCTCGGTGCGGCAATGCGGCTGCCAAGCGGAAT 240
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421 AAAAGTATGATCGTATCAATATAAATATGTCGCGGCGGATATGTTTATAGATATGGA 480
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DB 481 ACAGATGAAATCGAACAGAACTCAGGCGGTAAAGCGGTTACCCACCGCTTAGGTTATGAC 540
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DB 841 GAAACCAAAACCATGATGCGCAAGCTGATTAATAAATCAGTATGTCGCAATATAAAGAT 900
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QY	781	GATAACAAACCATGAAATGGCAAGCTGATTAATAATCAGTATGTCGAAATAAAAAAGAT	840
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2161	Db		GTTCA	AGCTG	ATGTT	TGGCA	ACAC	AGTTAG	AACTG	ATGAGT	TAAAC	2220
2221	QY		GTA	TTCCGT	CGCAAG	AAAG	TATG	CGAGG	AGGT	CGAAAA	TGA	2262
2221	Db		GTA	TTCCGT	CGCAAG	AAAG	TATG	CGAGG	AGGT	CGAAAA	TGA	2262

RESULT 3

BD074758	222 bp	DNA	linear	PAT 27-AUG-2000
DEFINITION	Neisseria lactoferrin-binding protein.			
ACCESSION	BD074758			
VERSION	BD074758.1	GI:22620361		
KEYWORDS	JP 2001514894-A/4.			
SOURCE	unidentified			
ORGANISM	unidentified			
REFERENCE	1. (pages 1 to 2262)			
AUTHORS	Fehlholm,A.M.P. and Thomsen,J.P.M.			
TITLE	Neisseria lactoferrin-binding protein			
JOURNAL	Patent: JP 2001514894-A 4 18-SEP-2001;			
	UNIVERSITY OF UTRECHT TECHNOLOGY FOUNDATION			
COMMENT	OS Unidentified			
	PN JP 2001514894-A/4			
	RD 18-SEP-2001			
	PP 10-AUG-1998			
	PR 15-AUG-1998	GB 9717423.9, 05-FEB-1998 GB 9802544.8 PI		
	ANICA MARGARETA PETERSON FEHLHOLM, JOHANES PETRUS MARIA PI			
	THOMSEN			
	PC C12N15/09,A61K39/095,A61K39/395,A61K48/00,A61P31/12,C07K14/22,			
	PC C07K16/12,			
	PC C12N1/21,C12P21/02,C12P21/08,G01N33/15,G01N33/50,G01N33/68,			
	C12N15/00			
	CC Strandedness: Double;			
	CC Topology: Linear;			
	CC Neisseria lactoferrin-binding protein			
	FH Key	Location/Qualifiers		
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CDS	8448..8759	/gene="NMB1544"	/note="hypothetical protein; identified by Glimmer2; putative"	QY	241	ATCGCAACTTTTGTATATAAAATGCTAATGAATATCCCAATAGTAAGCAGGACAGAGTAT	300
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				QY	301	CTGCGGCTCAAGAGAGAGATATCTGTGTTTATAGACGTTACGCGGAAAGAACAGGCTGAC	360
				Db	5544	CTGCGGCTTAAGAGAGAGATATCTGTGTTTATAGACGTTACGCGGAAAGAACAGGCTGAC	5485
				QY	361	AAACTTTAAAAGAAATCAACGACGSCATCTTAATGCACCAATCTACACGTCGGATTTA	420
gene	8763..8963	/gene="NMB1545"	/note="hypothetical protein; identified by Glimmer2; putative"	Db	5484	AAACTTTAAAAGAAATCAACGACGSCATCTTAATGCACCAATCTACACGTCGGATTTA	5425
				QY	421	AAAGATGATCGGATCAATATATAATATGTCGCGGCGGATATCTTTATATAGATATGGA	480
CDS	8763..8963	/gene="NMB1545"	/note="hypothetical protein; identified by Glimmer2; putative"	Db	5424	GAAGAGAAATATCAATATCAATTTGTCGCGGCGGATATCTTTATAGATATGGA	5365
				QY	481	ACA-----GATCAATCGAAGTCAAGCACTCAGCGGTAAGCGGTTACCAACCGCTTAGGT	534
				Db	5364	GGAAAGATATGAAAGAAAGAAAGACTTCTGATGTAGAGGTTTCTTAACCGATTAGT	5305
				QY	535	TATGACGGTTTGTATATTTATTCGAGAGAACTCTTCCCAATCTTTACGAGTGGGGA	594
				Db	5304	TATGACGGTTTGTATATTTATTCGAGAGAACTCTTCCCAATCTTTACGAGGCGGGA	5245
gene	9146..9430	/gene="NMB1546"	/note="hypothetical protein; identified by Glimmer2; putative"	QY	595	ACGGTGGATATCTCGTAACTGGCAATATATGACCGATGCCAAACGTCATCGAGCAGGT	654
CDS	9146..9430	/gene="NMB1546"	/note="hypothetical protein; identified by Glimmer2; putative"	Db	5244	ACGGTGGATATCTCGTAACTGGCAATATATGACCGATGCCAAACGTCATCGAGCAGGT	5185
				QY	655	CAGGCGTTGGCAATGACAAATTTGGTTATATACATTTATGTTGTAACGATTTGGTGA	714
				Db	5184	RAGGCGTTTTCAGTACGATTTGGTTATATACCAATATTTGTAATGAAATGGGCA	5125
				QY	715	ACTTCTTATGCGGCTAAGATGTCAGCAAGGAAAGACATCTCCCAATATGTAATACGTT	774
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				QY	775	GATTTGTATAACAAACCATGAATGGCAAGCTGATTAATAAATCAGTATGTGCAATAAAA	834
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				QY	835	A-----AAGATGAACCCCAAAACCGCTGACCAATTTACGACATTTGCAAAATTTGAC	888
				Db	5004	AGTAATCAAAATGAGCCCAAAACCGCTGACCAATTTACGACATTTGCAAAATTTGAC	4945
				QY	889	GGCAACCGCTTTACGCGCAGTGCAGTCAATCTGATTTAGCGGAAACCTTTGCCGCT	948
				Db	4944	GGCAACCGCTTTACGCGCAGTGCAGTCAATCTGATTTAGCGGAAACCTTTGCCGCT	4885
				QY	949	AATGAGGCTTTGTTTTCATGCGCATGCCGATCAGCGGCTTGAGGCGGCTTTTTCGCG	1008
				Db	4884	AAAGATATTTGTTTTCATGCGCATGCCGATCAGCGGCTTGAGGCGGCTTTTTCGCG	4825
				QY	1009	GATAACGAGAGAGCTTGGCGGACGCTTTATCAGCAACGACACACAGCTATTCGGGTA	1068
				Db	4824	GATAACGAGAGAGCTTGGCGGACGCTTTATCAGCAACGACACACAGCTATTCGGGTA	4765
				QY	1069	TTGCGAGGCA---AAAAACAGAGACAGCAAAACGACAGATACAAACCTTCGCTCCG	1125
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				Db	4644	AAAAATCCCGTGAAGTTGCGATTTCTATGCCGATTTTGGTCAATCCGCAAACTT	4585
				QY	1246	CTTGTGAGGGGCTGAATTTCTTTGGTAAACGAAACAAATCATCAAGCTTGGCGAC	1305
				Db	4584	CTTGTGAGGGGCTGAATTTCTTTGGTAAACGAAACAAATCATCAAGCTTGGCGAC	4525
				QY	1306	GGCAGGAAATGACCGTCCGTGCTTGTGCGATCTTTTACCTATGTAACCTCGGACGG	1365

ORIGIN

Query Match	68.9%	Score 1558;	DB 1;	Length 9955;
Best Local Similarity	83.6%;	Pred. No. 0;		
Matches 1906;	Conservative	0;	Mismatches 290;	Indels 84; Gaps 9;
QY	1	ATGTGTAACCGAATTTATGGCGCATGCTCTGTTGTTGCTTACCTTTAGCATCTGTATC	60	
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QY	61	GGCGGCAATTTCCGCGTACAGCTGTTGTGCAATCAAGCGGACGCGCCAACTCTGTCA	120	
Db	5772	GGCGGCAATTTCCGCGTACAGCTGTTGTGCAATCAAGCGGACGCGCCAACTCTGTCA	120	
QY	121	GATTCGAATCTTCCAAATCTCGGATAAGCCTCTCCAGCTCTGCGGACGCTTCGGTA	180	
Db	5724	TACCCGCTCACTTCAAACTTAAGGACGTTCCCACTCGGCCCTCGCGGCTCTTCGGTA	5665	
QY	181	GAATACGCGGCTCAAGCGGCGCGCTGCGTGGGCAATCGGCTGCCAAGCGGAAT	240	
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Db 98773 ACTTCTTATAGGCTTAGGATGTCGACGAAGGAAAAAGCATCTGCGCAATATACGGTT 98714
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QY 1306 GCGAGGAAATGACCGCTGCTGTTGCGACTTTTGGCTATGTAACGAGGAGGATCAAGAG 1425
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QY 1366 ATAAACCGATCGCGCGGAGTAACCAAGCGGAGAGTAAGGAGGAGGATCAAGAG 1425
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QY 1903 GCGAAGATTTGATGCGCAACCGTTTCCAGCGCAACGCGCGCTCGGAGAGCGGATCAAT 1962
Db 97606 GCGAAGATTTGATGCGCAACCGTTTCCAGCGCAACGCGCGCTCGGAGAGCGGATCAAT 97547
QY 1963 CTTTCCGGGAAATGTTTCGACCGACCCCAAAACCTTCCAGCTAGTAATCTTCCGTTAGAA 2022
Db 97546 CTTTCCGGGAAATGTTTCGACCGACCCCAAAACCTTCCAGCTAGTAATCTTCCGTTAGAA 2022
QY 2023 GAGAGATTTTACGCGCGCGGCGGAGTAATTTGGCGGTACTATTTTCAATATGATGGG 2082
Db 97486 GCGGAGATTTTACGCGCGCGGCGGAGTAATTTGGCGGTACTATTTTCAATATGATGGG 97427
QY 2083 AATCTCTTAGTATTAATGAAATATTTGAAATGAACTGAACTGAACTGAACTGAACTGAA 2142
Db 97426 AATCTCTTAGTATTAATGAAATATTTGAAATGAACTGAACTGAACTGAACTGAACTGAA 2142
QY 2143 GCTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 2202
Db 97384 GTTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 97328
QY 2203 AAACCAAAATTCGCGCTGATTTCCGTCGAGAAAGATATTCGAGAGGTGAAAAATGCA 2262
Db 97327 AAACCAAAATTCGCGCTGATTTCCGTCGAGAAAGATATTCGAGAGGTGAAAAATGCA 97268
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RESULT 6
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LOCUS
DEFINITION
2277 bp DNA linear BCT 07-FEB-1998
Neisseria meningitidis lactoferrin binding protein B (lbpB) gene,
complete cds.
ACCESSION
AF022781
VERSION
AF022781.1 GI:2843172
SOURCE
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 2277)
Petersson,A., Prinz,T., Umar,A., van der Biezen,J. and
Tomassen,J.
REFERENCE
AUTHORS
TITLE
Molecular characterization of LbpB, the second lactoferrin-binding
protein of Neisseria meningitidis
Mol. Microbiol. 27 (3), 599-610 (1998)
JOURNAL
MEDLINE
98149315
PUBMED
9489671
REFERENCE
2 (bases 1 to 2277)
Petersson,A., Prinz,T., Umar,A., van der Biezen,J. and
Tomassen,J.
TITLE
Direct Submission
Submitted (04-SEP-1997) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
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Qy	841	GAACCCAAAACCCGCTGACCATTTACGACATTAATGCAAAATGAGCGGCAACCGCTTTT	900
Dd	919	GAGAAGCAAAAACCGCTGACCATTTACAACTCATCTCGCATTTAAACCGCAACCGCTTT	978
Qy	901	ACCGCAGTGCACAGGTCAATCTCTGATTTAGCGAAAACTTGCCTGCTTAATGAGCGTTTG	960
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Qy	961	TTTTTCCATGCGATGCGGATCAGCGGCTTGAAGGCGGTTTTTTCGGCGATAACCGAGAA	1020
Dd	1039	TTTTTCCATGCGGATGCGGATCAGCGGCTTGAAGGCGGTTTTTTCGGCGATAAGGGGAA	1098
Qy	1021	GAGCTTGGCGGACGGTTTATCAGCAACGACACGCTATTTCGGGCTATTTCGACGCAAA	1080
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Dd	1642	GGCGGTTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1701
Qy	1681	TTCTTGAAGGATTCGCGACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1740
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Qy	181	GAAATCACCGCGTCAAGCGGCGCGCGTGGTGGGCGAATGGGCTGCGGCGGAGT	240
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Qy	241	ATCGCACTTTTGAATAAATGTAATGAAATCCCAATAGTAAGCAGGAGGAGTAT	300
Dd	328	ACTGCTTTTTCATCGTGAAGATGCAACGAAATTCGAAATGCAAGCAGGAGGAGTAT	387
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ORIGIN

Query Match 64.8%; Score 1465.2; DB 1; Length 2277;
Best Local Similarity 81.1%; Pred. No. 2.5e-304;
Matches 1835; Conservative 0; Mismatches 343; Indels 84; Gaps 8;

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 Db 1822 GAAGCGGCAAAAGCAGTATTTACCGTTGATTTCCGCAAGAAATCGATTTCCGAAAGCTG 1881
 QY 1861 ACGGAGCAAAACCGCGTAGAACCTGCTTTCCAAATTTGAAGACGCAAGATTTGATGCAAC 1920
 Db 1882 ACGGAGCAAAACCGCGTAGAACCTGCTTTCCAAATTTGAAGACGCAAGATTTGATGCAAC 1941
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 Db 2002 ACCGACCCCAAAACATTCCAGCTAGTAATCTTCGTGTAGAACGAGGATTTTACGCGCG 2061
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 Db 2122 GAAGTACTGAAATGAAGTTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 2181
 QY 2161 GTTGAAGCTGATTTGGCAACAGTGTAGAACCTGATGAAGTTAAACACAAATTTCCGCGTG 2220
 Db 2182 GCTGATGCTGATGTTG---AACAGTTAAAC---TGAAGTTAAACCCCAATTTCCGCGTG 2235
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RESULT 7
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 VERSION A98968.1 GI:6781928
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 SOURCE
 ORGANISM
 Neisseria meningitidis
 Neisseria meningitidis
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 Neisseriaceae; Neisseria.
 1 (bases 1 to 2277)
 Pettersson-Fernholm A.M. and Tommassen, J.P.
 NEISSERIA LACTOPERRIN BINDING PROTEIN
 Patent: WO 9909176-A 1 25-FEB-1999;
 JOURNAL UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIKA MAR (NL)
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 AQDESDIDINGESEDGEDEADGEDEEDATEDEDEDEDEDEDEDEDEDEDEDEDEDEDE
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ORIGIN
 Query Match 64.8%; Score 1465.2; DB 6; Length 2277;
 Best Local Similarity 81.1%; Pred. No. 2.5e-304;
 Matches 1835; Conservative 0; Mismatches 343; Indels 84; Gaps 8;

QY 1 ATGTGTAAACCGCAATATATGCGCGCATTTGCTGTTGCCCTTACTTTTAGCATCTTTGATC 60
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 QY 61 GCGGCAATTTGCGCGTACAGCCCTGTTGTCGAATCAACGCCGACCGCGCAACTCTGTCA 120
 Db 160 GCGGCAATTTGCGCGTACAGCCCTGTTGTCGAATCAACGCCGACCGCG----- 207
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 Db 208 TACCCCGTCACTTTCAAGTCTAAGGACGTTCCCACTCCGCCCTTCCCAACTTCTATA 267
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 Db 328 ACTGCTTTTTCATCGTGAAGTGGCAGCGAAATTTCCAAATAGCAACAAGCAAGAAAG 387
 QY 301 CTGCGCTCAAAAGAGAGATATCTCTGTTTTCAGCGGTACGCGGAAAGCAAGCGCTGAC 360
 Db 388 CTGCTGTTTCAAGAGGATGATGTTCTGTTTATACGGTTCAAAAGGAATAAATCTCAA 447
 QY 361 AAATTTAAAGGAAATCAAGCGCGCATCTTAATGCAACCAATCTACAGCTCCGATTTA 420
 Db 448 CAACTTTAAAGCGAAATTTCAATAACGATTCGATTCGATAGTAATTAGGACATCAGAAAAG 507
 QY 421 AAAGATGATGCGTATCAATATAAAATATGTCGCGCGCGGATATGTTTATATAGATATGSA 480
 Db 508 GAAATAAAATATGATTTAATTTGTAGATGAGGTTATGATATA---TGTAAGGGA 564
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 QY 541 GGTTTGTATATATTCGCGAGAACGTCCTTCCCAATCTTTACGAGTGGCGGAACGGTG 600
 Db 625 GGTTTGTATATATTCGCGAGAACGTCCTTCCCAATCTTTACGAGTGGCGGAACGGTG 684
 QY 601 GAATATTCTGTAACTGCGCAATATATACCGCATATATGCGCAAAACGTCATCGAGCAGGTCAGGCG 660
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 Db 745 GTTGGCATTCACAATTTGGGTTATATCACATTTTATGTTATGTTTATGTTGTCGAATCTCT 804
 QY 721 TATCGCGCTAAGGATGTCGACGAAAGGAAAGCAATCTCTGCGCAAAATATACGTTGATTTT 780
 Db 805 TATCGCGCTAAGGATGTCGACGAAAGGAAAGCAATCTCTGCGCAAAATATACGTTGATTTT 864
 QY 781 GATAACAAAACCAATGATGCAAGCTGATTAATAAATCAGTATGTGCGCAAAATATAAAGAT 840
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 Db 919 GAGAACCAAAAACCGCTGACATTTACCAATCTCACTGCGCATTTAAACCGCAACCGCTTT 978
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[illegible]

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Qy	301	CTGCCGCTCAAGAGAGAGATATCCTGTTTATTAGACGGTAGCGCCGAAAGAACAGGCTGAC	360
Db	388	CTGTCGTTTCAAGAAGGTGATGTTCTGTTTATTATACGGTTCAAAAGGAATTAACCTTCAA	447
Qy	361	AAACTTTAAAAAGGAAATCAACGACGGCATCTTAATGACCAATCTACAGTCGCGATTTA	420
Db	448	CAACTTTAAAGCGAAATCATTAACGTGATTCGATGTAGAAATTAGGACATCAGAAAG	507
Qy	421	AAAGATGATCGGTATCAATATAAATATGTCGCGCGGATATGTTTATACTAGATATGGA	480
Db	508	GAAAAATAAAAAATATGATTATAAATTTGTAGATGAGGTTATGTATA---TGTAAGGGA	564
Qy	481	ACAGATGAATCGAACAGAACTCAGCGGTAAGCGGTTACCCACCGCTTAGTTATGAC	540
Db	565	AAAGATGAAATTAAGTGGACTTCAGATTACAAGCAGTTTCCAACCGCTTAGTTATGAC	624
Qy	541	GGTTTTGTATATTATTCGCGAGAACGTCCTCCCTCCCAATCTTTACCGAGTCGGGAAACGGTG	600
Db	625	GGTTTTGTATATTATTCGAGAGACGTCCTCCCAATCTTTACCGAGTCGGGAAACGGTG	684
Qy	601	GAATATCTGTGTAACTGGCAATATATGACCGATGCCAAGCTCATCGACAGGTACAGCG	660
Db	685	GAATATCTGTGTAACTGGCAATATATGACCGATGCCAAGCTCATCGACAGGTAAAGCG	744
Qy	661	GTTCGCATGCAATTTGGTTTATATCATTTTATGTAAACGATGTTGGTCAACTTCT	720
Db	745	GTTCGCATGCAATTTGGTTTATATCACATTTTATGGTAAACGATGTTGGTCAACTTCT	804
Qy	721	TATCGCGTTAAGGATGTCGACGAAGGGAAGAGCATCTGTCGCAAAATATACGTTGATTTT	780
Db	805	TATCGCGTTAAGGATGTCGACGAAGGGAAGAGCATCTGTCGCAAAATATACGTTGATTTT	864
Qy	781	GATTAACAAAAACCATGAATGGCAAGTGAATAAAAATCAGTATGTGCGAAATATAAAAAAGAT	840
Db	865	GGTAACAAAAACCATGAATGGCAAGTGAATAAAAACCAATATGT-----CAAAACCCAGT	918
Qy	841	GAACCCAAAAACCGCTGACCAATTTACGACATTACTCGCAAAATTTGGACGCAACCGCTTT	900
Db	919	GAGAAGCAAAAACCGCTGAACATTTACAACATCACTGCCGATTTAAACCGCAACCGCTTT	978
Qy	901	ACCGCAGTGCACAGGTCAATCTCGATTTAGCGAAAACCTTCGCGGTATAGCGTTG	960
Db	979	ACCGCAGTGCACAGGTCAATCTCGATTTAGCGAAAACCATGCGCAATTAAGGAGCATTTG	1038
Qy	961	TTTTTTCATGCGATGCGATCAGCGCTTTGAGGGCGGTTTTTTTCGCGCAATAACGGAGAA	1020
Db	1039	TTTTTTCATGCGATGCGATCAGCGCTTTGAGGGCGGTTTTTTTCGCGATAGGGGGAA	1098
Qy	1021	GAGCTTCGCGACGGTTTATCAGCAACGACAAACAGCGTATTCGGCGTATTCGAGGCAAA	1080
Db	1099	GAGCTTCGCGACGGTTTATCAGCAACGACAAACAGCGTATTCGGCGTATTCGAGGCAAA	1158
Qy	1081	AAAAACGAGACAGCAAAACGACGAGATACAAAAACCTTCGCTCCGCTCGGAAACACACC	1140
Db	1159	CA-----AAATAGCCCGTCCCGTCTGAAACACACC	1191
Qy	1141	AAAATCTTGATTTCTTAATAAATTCGGTTGACGGCGACATGATGCCATGCCCGTAAG	1200
Db	1192	AAAATCTTGATTTCTCTGAAAAATTCGGTTGATGAGGCAAGTGTGAAATCCCCGACCG	1251
Qy	1201	TTTGCCATTTCTCTAGCCCGATTTTGGTCATCCGACAAACTCTTCTGCGAAGGGCGT	1260
Db	1252	TTTGCCATTTCTCTATGCCCCGATTTTGGTCATCCCGACAAACTCTTCTGCGAAGGGCAT	1311
Qy	1261	GAAATTCCTTTGGTAAACGAAGAAACAAATCATCAAGCTTTCGCGACGGCAGGAAATGACC	1320
Db	1312	GAAATTCCTTTGGTAGCCAGAGAAACCATCGAGCTTCCGACGGCAGGAAATGACC	1371

QY	1321	GTCCGTGCTTGTTCGCACTTTTTCGACTTAATGTGAAACTCGGACGGATATAAAACCGGATCGC	1338
Db	1372	GTCAGTGCTGTTGTTCGCACTTTTTCGACTTAATGTGAAACTCGGACGGATATAAAACCGGATCGC	1431
QY	1381	CCGCAAGTAAACCAAGGCGGAGATAAAGGGAGGATGAAGAGGTTGACGCGTTGAT	1440
Db	1432	CCCGCCGCAACCGAAGGC-----GAGGACGAAGAGGATTCGGACATTGAT	1479
QY	1441	AACGACGAAGAAACCGGAAGACGAAGCGGTGAAGACGAAGCGGCGGCGAAGACGAAACT	1500
Db	1480	AATGGCCGAAGAACGCAAGACGAATCGCGATGAAGAAGGAGGACCGAAGATGCAGCC	1539
QY	1501	TCCGAAGAGGANTATGCGAGACGGAAGAACCAACCGCCGAAGAAGAAACCCGAAGAAGTT	1560
Db	1540	GCAGGAGATGAAGCGACGAAGAAGACGAAGCCAC-----AGAAAC	1581
QY	1561	GATGAGCCGAAGAGGAGGAGTTGAAGAACCCGAAGAAATCGCCGGCAGAAGCGAAC	1620
Db	1582	GAAGACGGCAAGAAAGACGAAGCTGAAGAACTTGAAGAAGTAATCGTCGCAAGAGCGAAC	1641
QY	1621	GGCGGTTTCAGCGACATCTTCGCTGCCCTAGAACCTCTTAAAGCAGGACATCGACCTT	1680
Db	1642	GGCAGTTCAAACGCCATCTTCGCTGTCCCGAGACCTCTTAAAGCAGGATATCGACCTT	1701
QY	1681	TTCTCTGAAGGTATCCGACGGCAGAAACGGATATTCGCAAGCGGAAACGGCGCATTAT	1740
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QY	1741	ACCGGCACTTGGGAAGCGGTATCGGCACAAACCATTCATATGGGCAATTCAGCGCGATGAA	1800
Db	1762	ACCGGCACTTGGGAAGCGGTATCGGCACAAACCATTCATATGGGCAATTCATCGCGATAAA	1821
QY	1801	AAAGCGCAAAAGCAGAAATTTACGTTGATTTCCGACAAGAAATCGATTTCCGGAAGCTG	1860
Db	1822	GAAGCGCAAAAGCAGTAATTTACGTTGATTTCCGCAAGAAATCGATTTCCGGAAGCTG	1881
QY	1861	ACGGAGCAAAACGGCGTAGAAACCTGCTTCCATATTTGAAGACGGCAAGATTTGATGGCAAC	1920
Db	1882	ACGGAGCAAAACGGGTAGAAACCTGCTTCCGTTATTTGAAACCGCGTGAATGAGGGCAAC	1941
QY	1921	GGTTTTCCACGCGACAGCGGCACTCGGAGAGCGGCATCAATCTTTCGGGAATATGTTCTG	1980
Db	1942	GGTTTCCATGCAACAGCGCGCACTCGGATGACGGCATCGACCTTTCCGGCGAGGTTCTG	2001
QY	1981	ACCGACCCCAAAACATTTCCAGCTAGTATCTTCTGTGAGAAGGAGATTTTACGGCCCG	2040
Db	2002	ACCAACCGCAGATCTTCAAAGCTAATGATCTTCTGTGAGAAGGAGATTTTACGGCCCG	2061
QY	2041	CAGCGCGGGAATTTGGCGGTACTATTTTCAATAATGATGGGAATCTCTTAGTATAACT	2100
Db	2062	AAGCGGAGGAATTTGGCGGTATTTATTTTCAATAATGATGGGAATCTCTTAGTATAACT	2121
QY	2101	GAATAATTTGAAATTTGAAGCTGAAGCTGAAGTTGAAGTTGAAGCTGAAGTTGAA	2160
Db	2122	GAAGTACTGAATAATAAGTTTGAAGCTGATTTGATTTGATTTGATTTGATTTGATTTGAT	2181
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QY	2221	GTATTCGCTCGGAAGAGATATCGAGGAGTGGAAATGA	2262
Db	2236	GTATTCGCTCGGAAGAGATATTAAGAGGTTGAAATGA	2277

RESULT 9

AF049349

LOCUS

DEFINITION

1
2
3
4
5
6
7
8
9

ACCESSION
NUMBER

VERSION

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Db 1118 GGTTTTGATATATATTCGGAGAACGTCCTTCCCAATCTTTACCGAGTGGGGAACGGTG 1177
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Qy 1981 ACGGACCCCAACATTCGAGCTAGTAACTCTTCTGTAGAGAGGATTTTACGCGCG 2040
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RESULT 10

AF031432

LOCUS

DEFINITION

Neisseria meningitidis

precursor (lbpB) gene, complete cds.

ACCESSION

AF031432

VERSION

AF031432.1

KEYWORDS

SOURCE

ORGANISM

Neisseria meningitidis

Neisseria meningitidis

Bacteria; Proteobacteria;

Neisseriaceae; Neisseria.

1 (bases 1 to 2537)

Bonnah, R.A. and Schryvers, A.B.

Preparation and characterization of Neisseria meningitidis mutants

deficient in production of the human lactoferrin-binding proteins

lbpA and lbpB

J. Bacteriol. 180 (12), 3080-3090 (1998)

2537 bp DNA linear BCT 12-JUN-1998

GI:3213214

Neisseria meningitidis

Neisseria meningitidis

Bacteria; Proteobacteria;

Neisseriaceae; Neisseria.

1 (bases 1 to 2537)

Bonnah, R.A. and Schryvers, A.B.

Preparation and characterization of Neisseria meningitidis mutants

deficient in production of the human lactoferrin-binding proteins

lbpA and lbpB

J. Bacteriol. 180 (12), 3080-3090 (1998)

Thu Aug 26 10:18:17 2004

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MEDLINE 98292739
PUBMED 9620956
REFERENCE 2 (bases 1 to 2537)
AUTHORS Bonnah,R.A. and Schryvers,A.B.
TITLE Direct Submission
JOURNAL Microbiology & Infectious Diseases,
Submitted (24-Oct-1997) 3330-Hospital Drive N.W., Calgary, AB T2N
4N1, Canada

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    mat_peptide
        Query Match 64.7%; Score 1463.6; DB 1; Length 2537;
        Best Local Similarity 81.1%; Pred. No. 5.6e-304;
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        181 GAAATCACGCGGTCAACGGCGCCCGCGTGGTGGCGCAATCGCGTCCCAAGCGGAAT 240

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301 CTGCGGCTCAAGAGAGAGATATCTGTTTGTAGACGGTACCGGAAAGAACAGGCTGAC 360
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541 GGTGTTGTATATTTATTCGGAGAACGTCCTTCCCAATCTTTACCGAGTCCGGAGACGGTG 600
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COMMENT
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Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C.,
Klee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T.,
Davies, R.M., Davis, P., Devlin, K., Feltwell, T., Hamlin, N.,
Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K.,
Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M.,
Skellton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G.
Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491
Nature 404 (6777), 502-506 (2000)
20222556
10761919
2 (bases 1 to 326301)
Parkhill, J.
Direct Submission
Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
Notes:
Details of N. meningitidis sequencing at the Sanger Centre are
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
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ACCESSION
AF123380
VERSION
AF123380.1 GI:4884686

2226 bp DNA linear BCT 24-MAY-1999

KEYWORDS

SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE 1 (bases 1 to 2226)
AUTHORS Pattersson,A., van der Biesen,J., Joosten,V., Hendriksen,J. and Tomassen,J.

TITLE Sequence variability of the meningococcal lactoferrin-binding

protein lbpB

Gene 231 (1-2), 105-110 (1999)

JOURNAL MEDLINE

99250255

REFERENCE PUBMED

10231574

AUTHORS Pattersson,A., van der Biesen,J., Joosten,V., Hendriksen,J. and Tomassen,J.

TITLE Direct Submission

Submitted (26-JAN-1999) Department of Molecular Cell Biology,

Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands

FEATURES

source

gene

CDS

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ORIGIN

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 Neisseriaceae; Neisseria.
 REFERENCE 1 (bases 1 to 2226)

AUTHORS
TITLE
JOURNAL

Pettersson-Fernholm, A.M. and Tommassen, J.P.
 NEISSERIA LACTOFERRIN BINDING PROTEIN
 Patent: WO 9909176-A 5 25-FEB-1999,
 UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIKA MAR (NL)

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ORIGIN

Query Match 63.8%; Score 1442.2; DB 6; Length 2226;
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DEFINITION				linear
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SOURCE ORGANISM

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1. (Dase, I. C. 2220),
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AUTHORS
FELDMAN, A.M.F. and THOMPSON, C.F.

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PN 2001314894-A/3

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PF 10-AUG-1998 JF 2000309840

PR 15-AUG-1997 GB 9/1/423.9, 03-FEB-1998

ANICA MARGARETA PETERSON FELNHOLM, JOHN

THOMASSEN

PC C12N15/09, A61K39/095, A61K39/395, A61K39/395

PC C07K16/12,

PC C12N1/21, C12P21/02, C12P21/08, G01H

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2017	GGCTTTTACGCGCCGACGCGGAGNATTTGGCGGTACTATTTTCAATAATGATGGGAAA	2076
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ACCESSION	AF072890	(lbpB) gene, complete cds.
VERSION	AF072890.1	GI:4106392
KEYWORDS	Neisseria gonorrhoeae	
SOURCE	Neisseria gonorrhoeae	
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.	
REFERENCE	1 (bases 1 to 2519)	
AUTHORS	Biswas, G.D., Anderson, J.E., Chen, C.J., Cornelissen, C.N. and Sparling, P.F.	
TITLE	Identification and functional characterization of the Neisseria gonorrhoeae lbpB gene product	
JOURNAL	Infect. Immun. 67 (1), 455-459 (1999)	
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TITLE	Direct Submission	
JOURNAL	Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521 Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA	
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Best Local Similarity 80.7%; Pred. No. 1.7e-297; Indels 81; Gaps 10;			
Matches 1828; Conservative 0; Mismatches 356;			
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QY	481	ACAGATGAATCGAACAGAACTCAGCGGTGTAAGCGGTTACCCACCGCTTAGGTATGAC	540
Db	778	AAAGATGAATCGAACAGAACTCAGGTGTAAGCGGTTTACCCACCGCTTAGGTATGAC	837
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Job time : 8501.05 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:48:44 ; Search time 766.365 Seconds
(without alignments)
12538.967 Million cell updates/sec

Title: US-10-735-098-7
Perfect score: 2262
Sequence: 1 atgtgtaaaccgaattatgc

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseq1990s:*
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SUMMARIES

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		Match	%				
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C 2	1558	68.9	110000	3	AAAF1489_1	Continuation (2 of	
C 3	1558	68.9	34980	3	AA21611	Aaf21611 Neisseria	
4	1465.2	64.8	2277	2	AAX23319	Aax23319 N. mening	
5	1442.6	63.8	2226	7	ACA41945	ACA41945 Prokaryot	
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7	1291.8	57.1	2124	2	AAX23323	Aax23323 N. mening	
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C 9	1100.2	48.6	14652	4	AAAF1482	Aax81482 N. mening	
10	730	32.3	1000	4	AAF91389	Aaf91389 N. mening	
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13	169.2	7.5	3300	6	ABS67377	ABs67377 Neisseria	
14	102	4.5	963	5	AAAS69580	Aas69580 DNA encod	
15	99.2	4.4	400	5	AAAS75460	Aas75460 DNA encod	
16	95.4	4.2	708	5	AAAS69547	Aas69547 DNA encod	
17	95.4	4.2	708	5	AAAS75461	Aas75461 DNA encod	
18	95.2	4.2	372	5	AAAS75452	Aas75452 DNA encod	
19	95.2	4.2	1072	5	AAAS90738	Aas90738 DNA encod	
20	95	4.2	801	5	AAAS90729	Aas90729 DNA encod	
21	94.2	4.2	29392	2	AAV15422	AAv15422 Mouse pol	
22	93.4	4.1	379	5	AAAS90909	Aas90909 DNA encod	
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ALIGNMENTS

RESULT 1

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XX	XX	AA23322;
DT	DT	11-JUN-1999 (first entry)
XX	XX	
DE	DE	N. meningitidis strain M990 LbOb cDNA.

LbpB; lactoferrin binding protein; vaccine; neisserial disease;
 KW
 meningitis; diagnosis; treatment; ds.
 KW

xx
OS
Neisseria meningitidis.

Key	Location/Qualifiers
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AA PN WO9909176-A1.

PD 25-FEB-1999.

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PF
10-AUG-1998: 98WO-EP005117.

15-AUG-1997: 97GB-00017423

PR 05-FEB-1998; 98GB-00002544;

PA (UYUT-) RIJKSUNIV UTRECHT.

PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.

PI Pettersson-Fernholm AM, Tommassen JPM;

WPI; 1999-190165/16.

DR P-PSDB; AAW93495.

New lactoferrin-binding protein B polynucleotides - obtained from PPT Neisseria meningitidis, used to develop products for the diagnosis, PPT prevention and treatment of neisserial disease, e.g. meningitis. PPT

PS
Claim 2; Page 98-102; 116pp; English.

This invention describes novel lactoferrin-binding protein B (LbpB) strains of *Neisseria meningitidis*. The products of this invention are used for vaccinating humans against neisserial disease e.g. meningitis.

ne; neisserial disease;

apq 1000

TING ST.

CC Antibodies raised against the proteins of the invention can be used for
 CC diagnosing or treating neisserial disease in humans. The lbpB
 CC polypeptides can also be used for identifying compounds which inhibit the
 CC polypeptides

XX Sequence 2262 BP; 698 A; 487 C; 590 G; 487 T; 0 U; 0 Other;

Query Match 100.0%; Score 2262; DB 2; Length 2262;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	361	AAACTTAAAGAGAAATCAACGGCGATCTTAATGACCAATCTACACGTCGCAATTA	420
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Qy	421	AAAGATGATGCTATCAATAATAATATATGTCGGGCGGATATGTTTATAGTATGGA	480
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Qy	481	ACAGATGAATCGACAGAACTCAGCGGTAAAGCGGTATCCACCGCTTAGGTTATGAC	540
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Qy	841	GAACCCAAACCGCTGACATTTACGACATTTAGTCAAAATTTGACGCGCAACCGCTTT	900
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 QY 835 A-----AAGATGAACCCAAAACCGCTGACCAATTTACGACATTTACCGCAATTTGAC 888
 Db 98653 AGTAATCCAAATGAGCCCAAAAACCGCTGACCAATTTACGACATTTACCGCAATTTGAC 98594
 QY 889 GGCACCGCTTTACCGGAGTCCGACGATCTGATTTAGCGAAACACCTTCGCGGT 948
 Db 98593 GGCACCGCTTTACCGGAGTCCGACGATCTGATTTAGCGAAACACCTTCGCGGT 98534
 QY 949 AATGAGCGTTTGTCTTCCATGCCATGCCATCAGCGCTTTGAGGCGGTTTTTTCGGC 1008
 Db 98533 AAGAATATTTGTTTTCATACCGATCCGATCCGATCAGCGCTTTGAGGCGGTTTTTTCGGC 98474
 QY 1009 GATACGGAAGAGCTTCCGCGAGCTTTATACGACGACCAACAGCGATTTTCGGCGTA 1068
 Db 98473 GATACGGAAGAGCTTCCGCGAGCTTTATACGACGACCAACAGCGATTTTCGGCGTA 98414
 QY 1069 TTCCGAGCA---AATAACGAGACACCAACCGCAGCAGATACAAACCTTCGCGGTCCG 1125
 Db 98413 TTCCGAGCAACAAACAAACGAGACGAAACCGCAGCAGATACAAACCTTCGCGGTCCG 98354
 QY 1126 TCTGGAACACACCAAAATCTCGATTTCTCTAATAATTTCCGTTGACGAGCGCACTGAT 1185
 Db 98353 TCTGGAACACACCAAAATCTCGATTTCTCTAATAATTTCCGTTGACGAGCGCACTGAT 98294
 QY 1186 GGCATGCCGTAAAGTTTGCATTTCTCTATGCCCGATTTTGTCTATCCCGACAAACTT 1245
 Db 98293 AAAAATCCCGTGAGTTTGCATTTCTCTATGCCCGATTTTGTCTATCCCGACAAACTT 98234
 QY 1246 CTGTGCAAGGGCTGAAATTCCTTTGTAACGAGACCAAAATCATCAGCTTGCAGAC 1305
 Db 98233 CTGTGCAAGGGCTGAAATTCCTTTGTAACGAGACCAAAATCATCAGCTTGCAGAC 98174
 QY 1306 GGCAGGAAATGACCGTCCGTGCTTGTGCGACTTTTGTGACTATGTGAACTCGGACGG 1365
 Db 98173 GGTAGGAAACGCAATCCGAACTCTGCTGATTTCTGACTTATGTGAAATTCGACGG 98114
 QY 1366 ATAAACCGATCCCGGCAAGTAATACCAAGCGCAAGATAAAGGGGAGGATGAAGAG 1425
 Db 98113 ATGCAACCGAAGCTCCCGCGCAACCGAAGCGCAGACGAGAGAGAGAGAGAGAG 98054
 QY 1426 GGTGACGGCTTGATACGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1485
 Db 98053 GATACGCGCTTGATAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 97994
 QY 1486 GAAGAAGACGAACTTCCGAAGAGGATAATGGCGAAGCAGCAAGCAACCGCGAGAA 1545
 Db 97993 GAAGAG-----CAGCGTAAACAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 97955
 QY 1546 GAAACGAGAGTTGATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1605
 Db 97954 GAAGCGGTAGAGT-----GAAGATGAAGCTGAAGAACCCGAGAGAGAGATCG 97907

QY 1606 CCG---GCAGAGAGCAACGGCGGTTTCAGGACGATCCTGCCTGCTAGAGCTCTAAA 1662
 Db 97906 CCGCAGAGAGAGAGCGGCGACCGGTTTCAGACGCAATCTCCCGCTCCGAGAGCCCTAAA 97847
 QY 1663 GGCAGGACATCGACCTTTTCTGAAAGGTATCCGACCGGAGAAACGATATTCGCGAA 1722
 Db 97846 GGCAGGACATCGACCTTTTCTGAAAGGTATCCGACCGGAGAAACGATATTCGCGAA 97787
 QY 1723 ACGGGAACGGCGCATTTATACCGGCACTTGGGAGCGGCTATCGGCAACCCATTCATGG 1782
 Db 97786 ACTGGAAGACACTATACCGGCACTTGGGAGCGGCTATCGGCAACCCATTCATGG 97727
 QY 1783 GACAAATCAGGCGGATGAAAGAGCGGCAAAAGCAGAAATTTACCGTTGATTTCCACAAAGAA 1842
 Db 97726 GACAAATCAGGCGGATGAAAGAGCGGCAAAAGCAGAAATTTACCGTTGATTTCCGCAAGAA 97667
 QY 1843 TCGATTTCCGGAAGCTGACGAGCAAAACCGCGTAGAACCTGCTTCCATATTTGAAGAC 1902
 Db 97666 TCGATTTCCGGAAGCTGACGAGCAAAACCGCGTAGAACCTGCTTCCATATTTGAAGAC 97607
 QY 1903 GGCAGATTTGATGCAACGCTTCCACGCGACGCGCACTCCGAGAGCGGCATCAAT 1962
 Db 97606 GGCAGATTTGATGCAACGCTTCCACGCGACGCGCACTCCGAGAGCGGCATCAAT 97547
 QY 1963 CTTTCGGGAAATGTTTCGACCGACCCCAAAACATTTCCAAAGCTAGTAATCTTCGTGTAGAA 2022
 Db 97546 CTTTCGGGAAATGTTTCGACCGACCCCAAAACATTTCCAAAGCTAGTAATCTTCGTGTAGAA 97487
 QY 2023 GGAGATTTTACGCGCGCGCAGCGCGGCAATTTGGCGGTACTATTTTCAATAAGTATGGG 2082
 Db 97486 GGAGATTTTACGCGCGCGCAGCGCGGCAATTTGGCGGTACTATTTTCAATAAGTATGGG 97427
 QY 2083 AAATCTCTTACTATACTGAAATATTTGAAATGAACTGAACTGAACTGAACTGAACTGAA 2142
 Db 97426 AAATCTCTTACTATACTGAAATATTTGAAATGAACTGAACTGAACTGAACTGAA 97385
 QY 2143 GCTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 2202
 Db 97384 GTTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTT 97328
 QY 2203 AAACACAAATTCGCGGTGTTATTCGTTCCGAGAAAGATATSCAGAGAGGTGGAAGAAATGA 2262
 Db 97327 AAACACAAATTCGCGGTGTTATTCGTTCCGAGAAAGATATSCAGAGAGGTGGAAGAAATGA 97268

RESULT 4

AAX23319
 ID AAX23319 standard; cDNA; 2277 BP.
 XX AAX23319;
 AC AC
 XX XX
 DT 11-JUN-1999 (first entry)
 XX

N. meningitidis strain BNCV lbpB cDNA.

lbpB; lactoferrin binding protein; vaccine; neisserial disease; meningitis; diagnosis; treatment; ds.

Neisseria meningitidis.

Key Location/Qualifiers
 CDS 100..2277
 FT /*tag= a
 FT /product= "lbpB"
 XX

MO9909176-AL.

25-FEB-1999.

10-AUG-1998; 98WO-EP005117.

15-AUG-1997; 97GB-00017423.

apf/05

QY 1741 ACCGGCCTTGGGAAGCGCTATCGGCAAAACCCATTCATGCGACAAATCAGCGCGATGA 1800
 Db ACCGGCCTTGGGAAGCGCTATCGGCAAAACCCATTCATGCGACAAATCAGCGCGATGA 1821
 QY 1801 AAGCGCGCAAAACAGAGATTTACCGTTGATTTTCGACAAAGAAATCGATTTCCGGGAAAGCTG 1860
 Db GAAGCGCGCAAAACAGAGATTTACCGTTGATTTTCGACAAAGAAATCGATTTCCGGGAAAGCTG 1881
 QY 1861 ACGGAGCAAAACCGGCTAGACCTCTTCCATTTTGAAGACGGCAAGATTTGATGGCAAC 1920
 Db ACGGAGCAAAACCGGCTAGACCTCTTCCGTTATTTGAAGAAACCGGCTGATTTGAGGCGAAC 1941
 QY 1921 GGTTCACGCGACACGCGGCACTCGGAGAGCGGCATCAATCTTTTCGGGAAATGCTTCG 1980
 Db GGTTCACGCGACACGCGGCACTCGGATGACGGCATCGCTTTCCGGGCAAGGTTTCG 2001
 QY 1981 ACGGACCCCAAAACATTCAGCTAGTAATCTTTCGTTGAGAGGAGATTTTACGCCCG 2040
 Db ACCAAACCGCAGATCTTCAAGCTAATGATCTTCTGTTAGAGGAGATTTTACGCCCG 2061
 QY 2041 CAGCGCGCGGAATTCGGCGGTACTATTTTCAATATGATGGGAAATCTCTTAGTATACT 2100
 Db AAGCGCGGAGGAATTCGGCGGTATTTTCAATATGATGGGAAATCTCTTAGTATACT 2121
 QY 2101 GAAATATTTGAAATCAAGCTGAAGCTGAAGTTGAAGTTGAAGCTGAAGCTGAAGTTGA 2160
 Db GAAGTACTGAAATATAAGTTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 2181
 QY 2161 GTTGAAGCTGATTTGGCAACAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 2220
 Db GCTGATGCTGATTTGG---ACAGTTAAAC---TGAAGTTAAACCCCAATTCGCGCTG 2235
 QY 2221 GTATTCGCTGCAAGAAAGATATGAGGAGGTTGAAGTGA 2262
 Db GTATTCGCTGCAAGAAAGATATTAAGAGGTGGAAATGA 2277

RESULT 5

ACA41945
 ID ACA41945 standard; DNA; 2226 BP.
 XX ACA41945;
 AC ACA41945;
 XX 19-JUN-2003 (first entry)
 DT Prokaryotic essential gene #23602.
 DE Prokaryotic essential gene
 DE Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 KW Neisseria meningitidis.
 XX WO200277183-A2.
 XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITFA PHARM INC.
 PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI: 2003-029926/02.
 DR P-PSDB; ABUS8075.
 XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 14; SEQ ID NO 29815; 1766pp; English.
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

Sequence 2226 BP; 701 A; 466 C; 566 G; 493 T; 0 U; 0 Other;

Query Match 63.8%; Score 1442.6; DB 7; Length 2226;
 Best Local Similarity 80.3%; Pred. No. 0;
 Matches 1844; Conservative 0; Mismatches 349; Indels 102; Gaps 9;

QY 1 ATGTGTAAACCGAATTATGGCGCATTCCTCTGTTCCTTACCTTTAGCATCTTGATC 60
 Db 1 ATGTGTAAACCGAATTATGGCGCATTCCTCTGTTCCTTACCTTTAGCATCTTGATC 60
 QY 61 GGCGGCAATTCGCGGTACAGCTGTGTGCAATCAACGCGACCGCCCAACTCTGTCA 120
 Db 61 GGCGGCAATTCGCGGTACAGCTGTGTGCAATCAACGCGACCGCCCAACTCTGTCA 120
 QY 121 GATTCCAAATCTTCCAATCTCGGGATAAGCTCTCCAGCTCTCTCGGAGCCCTCGGTA 180
 Db 109 TACCCGCTCACTTCAAGCTTAAGGAGCTTCCCACTTCGCCCTCTCGCGGCTTCGGTA 168
 QY 181 GAAATACGCGCGGTCAAGCGCGCCCGCGTCTCGTGGCAATCGGCTGCCAAGCGCAAT 240
 Db 169 GAAACACGCGCGGTCAACCGCGCGCGTCTCGTGGCAATCGGCTTGTGAGCGCAAT 228
 QY 241 ATCGCAACTTTTGAATAAATGTAATAATCCCAATAGTAAGCAGGAGGAGTAT 300
 Db 229 ATTGCTTTTCATCGTGAAGATGCGCAATTCGCGCAATTCGCGCAATTCGCGCAAT 288
 QY 301 CTGCGCTCAAGAGAGGATATCTCTGTTTATAGCGGTACGCGCAAGACAGGCTGAC 360
 Db 289 CTGCTGTTTAAAGAGGTGATCTCTGTTTATAGCGGTTCGCGCAATTCGCGCAAT 348
 QY 361 AAACCTTAAAGAGGAAATCAACGCGCGCATCTCTTAATGCAACCAATCTACAGCTCGGATTA 420
 Db 349 CAGCTTAAAGGATAAATTCATCAACGCAATCTCTTAATGCAACCAATCTACAGCAAT 408
 QY 421 AAAGATGATCGGTATCAATATAAATATGTCGCGCGCGGATATGTTTATATAGATGGA 480

Dd	409	GAATAATATAAATAATGTTATGAAATTTGTAGATCGAGTTATGATATACATAAAGGGA	468
Qy	481	ACAGATGAAATCGAACAAGAACTCAGCGGGTTAAGCGGGTTACCCACCGCTTAGGTTATGAC	540
Dd	469	AAAGATGAAATTTGAGTGACATCAATCACAAGCAGTTTACCTACCGGTTTGGTTATGAC	528
Qy	541	GGTTTTGTATATTATTCGGAGAACGTCCTCCAAATCTTTACCGAGTCCGGGAACGGTG	600
Dd	529	GGTTTTGTATATTATTCGGAGAACATCTTTCCAAATCTTTACCGAGCGGGGAACGGTG	588
Qy	601	GAATATCTGTGTAATCTGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTCAGGC	659
Dd	589	AAATATTCGGCAACTGGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTAAGCA	648
Qy	660	--GGTTGGCATTGACAAATTTGGGTTATATCAATTTTATGTAACGATGTTGGTGCAACT	717
Dd	649	GGAGATCTCTAGCGAAGATTTGGGTTATATCGTTTATTACGGTCAAAATGTCCGGACAAT	708
Qy	718	TCTTATCGCGCTTAAGATGTCGACGAAGGGAAGAGCATCTGCCAAATATATACGGTTGAT	777
Dd	709	TCTTATGCTGCGACTGCGCAGCAGCCGAGAGGGAAGAACTCCGCCGAATATACGGTAGAT	768
Qy	778	TTTGATAACAAACCATGAATGGCAAGCTGATTTAAAAATCAGTATGTGCAAAATAAAAA	837
Dd	769	TTCCGTTAAGAAACTTTGACGGTTAAATTAATTAATAATCAGTATGTGCAAAAGAAACC	828
Qy	838	GATGAACCCAAAAAAACCGCTGACCAATTTACGATTTACGCAAAATTTGACCGCAACCGC	897
Dd	829	GATGAA---AGAAACCCGCTGACCATTTACGACATTTACTGCAACATTTGACCGCAACCGC	885
Qy	898	TTTACCGGAGTCCAAAGTCAATCTGATTTAGCGMAAAACCTTGCCTGTAATGAGCGT	957
Dd	886	TTTACCGGAGTCCAAAGTCAATCTGATTTAGCGMAAAACCTTGCCTGTAATGAGCGT	945
Qy	958	TTGTTTTTCCATGCGGATCCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCGATTAACGGA	1017
Dd	946	TTGTTTTTCCATGCGGATCCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCGATTAACGGA	1005
Qy	1018	GAAGAGTTGCGGAGCGGTTATACGACGACGACGAGGATTTGCGCGTATTTCCGCGATTAACGGA	1077
Dd	1006	GAAGAGTTGCGGAGCGGTTATACGACGACGACGAGGATTTGCGCGTATTTCCGCGATTAACGGA	1065
Qy	1078	A---AAAAACAGACAGCAACAGCAGCAGATACAAAACCTGCCCTCGCTCTGGAATA	1134
Dd	1066	AAAAAAACAGACGACGACGACGATCAGATACAAATCTGCTATGCGCTCTGGAATA	1125
Qy	1135	CACACCAAAATCTTGATTTCTTAAATAATTTCCGTTGACGAGCGGCTGATGCGCATGCC	1194
Dd	1126	CACACCAAAATCTTGATTTCTGATAATTTCCGTTGACGAGCGGCTGATGCAATGCC	1185
Qy	1195	CGTAAGTTGCGCATTTCTGATGCGGATTTTGGTCATCCCGACAAATCTTCTTGTGAA	1254
Dd	1186	CGTAAGTTGCGCATTTCTGATGCGGATTTTGGTCATCCCGACAAATCTTCTTGTGAA	1245
Qy	1255	GGCGGTGAATCTCTTTGTTAAACAGAAACAATCATCAAGCTTCCCGACGCGCAGAAA	1314
Dd	1246	GGCGGTGAATCTCTTTGTTCAAAAGATCTCAAAACCATCGATCTTCCCGACGCGCAGAAA	1305
Qy	1315	ATGACCGTCCGTCGTTGTTGCGACTTTTGAACCTATGTGAAATCTCGACGAGTAATAACC	1374
Dd	1306	ATGACCGTCACTGTTGTTGCGACTTTTGAACCTATGTGAAATCTCGACGAGTAATAACC	1365
Qy	1375	GATCGCGCGCAAGTAAACAAAGCGGGAAGA-----TAAA	1410
Dd	1366	GACCGCGCGCAAGTAAACAAAGCGGGAAGATGAAAATTTCCGAAGATGAAATTTGGTGAA	1425
Qy	1411	GGGAGAGATGAAGAGGTCGAGCGTTGATAACGACGAAGAAAGCGAAGCAAGCCGTA	1470
Dd	1426	AGCGAGGAAATGAGAGGATTTGGTCGCTGAAGAGAAACACGCGAAGCAGTCTGTA	1485
Qy	1471	GAGACGAAGCGCGCAAGAGACGAACCTTCCGAAGAGATTAATGCGCAAGCAGAAAGAA	1530
Dd	1486	GAAGATGAAGACAGAGAGAGAGCAAGTTTTCCGAAGATGTTTCCGAAGATGTTAAGCAGAAAGAA	1545

Qy	1531	GCAACCGCCGAAGAAGAAACCGAAGAAAGTTGATGAAGCCGAAGAGGAGAAAGTTGAAGAA	1590
Dd	1546	GAATCTCCCGNA-----GAAGATGATGATGAGCCGAAGAGGAGAAAGTTGAAGAA	1596
Qy	1591	CCCGAAGAAATAATCCCGCGCAAGAGCAAC---GGCGGTTCCAGGACGATCTGCTCTGCC	1647
Dd	1597	CCCGAAGAAATAATCCCGCGCAAGAGCGCGTGGCGGTTCCAGACGGCATCCCGCCCGCT	1656
Qy	1648	CTAAGAGCTCTAAGGCGAGGACATCGACCTTTTCTGAAAGGTATCCGACCGCGAAGAA	1707
Dd	1657	TCGGAAGCCCTTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATCCGACCGCGAAGAA	1716
Qy	1708	ACGATATTTCCGCAAGGCGAACCGCGCATTTATACCGGCATTTGGGAAGCGGTATCGGC	1767
Dd	1717	GCCGACATTCGCAAACTGGAAGACGCTATACCGGCATTTGGGAAGCGGTATCAGC	1776
Qy	1768	AAACCCATTCATGGGCAATCAGCGGATGAAAAGCGGCAAGAGCAATTTACCGTT	1827
Dd	1777	AAACCCATTCATGGGCAATTAAGCGGATTAAGAAAGCGGCAAGAGCAATTTACCGTT	1836
Qy	1828	GATTTTCGACAAAGATCGATTTTCGGAAGCTGACGAGCAAAACCGGCTAGAACCTGCT	1887
Dd	1837	GATTTTCGCGAAGAAATCGATTTTCGGAAGCTGACGAGCAAAACCGGCTAGAACCTGCT	1896
Qy	1888	TTCCATATTTGAAGACGCGCAAGATTTGATGGCAACCGTTTCCAGCGCAACGCGCACTCGG	1947
Dd	1897	TTCTATATTTGAAGAGGTGATGATGATGCAACCGTTTCCAGCGCAACGCGCACTCGG	1956
Qy	1948	GAGACGCGCATCAATCTTTTCGGGAAATGGTTCGACCGCAACCCCAAAACATTTCAAGCTAGT	2007
Dd	1957	GATTAACGCGCATCAATCTTTTCGGGAAATGGTTCGACCAACCCCAAAACATTTCAAGCTAGT	2016
Qy	2008	ATCTTCTGTTAGAGGAGGATTTTACGCGCCGCGAGCGCGCAATTTGGGCGGTACTATT	2067
Dd	2017	GATCTCTGTTAGAGGAGGATTTTACGCGCCGCGAGCGGAGATTTGGGCGGTACTATT	2076
Qy	2068	TTCAATATATGATGGGAAATCTCTTAGTATACTGATAAATATTGAAAATGAAGCTGAAGCT	2127
Dd	2077	TTCAATATGATGGGAAATCTCTTAGTATACTGATAAATATTGAAAATGAAGCTGAAGCT	2123
Qy	2128	GAAGTTGAAGTTGAAGCTGAAGCTGAAGTTGAGTTGAGCTGATGCTTGGCAAAACAGTTTA	2187
Dd	2124	-----TGAAATTTGAAGCTGATGCTGGCGAAACAGTTTA	2154
Qy	2188	GAACTGTAGAGTTAAACACAAATTTCCGCGTGGTATTCCGTCGCAAGAAAGATATGCGAG	2247
Dd	2155	GAACTGTAGAGTTAAACACAAATTTCCGCGTGGTATTCCGTCGCAAGAAAGATATGCGAG	2247
Qy	2248	GAGGTGGAAAAATGA	2262
Dd	2212	GAGGTGGAAAAATGA	2226

RESULT 6
AAAX23321
ID AAX23321 standard; cDNA; 2226 BP.
XX AAX23321;
AC AAX23321;
XX
DT 11-JUN-1999 (first entry)
XX
XX N. meningitidis strain H44/76 LbpB cDNA.
DE
XX
XX LbpB; lactoferrin binding protein; vaccine; neisserial disease;
KW meningitis; diagnosis; treatment; ds.
XX
XX Neisseria meningitidis.
OS
XX
XX Key Location/Qualifiers
PH 1. 2226
FT /*tag= a
FT /product= "LbpB"

XX WO9909176-A1.
 XX 25-FEB-1999.
 XX 10-AUG-1998; 98WO-EP005117.
 XX 15-AUG-1997; 97GB-00017423.
 XX 05-FEB-1998; 98GB-00002544.
 XX (UYUT-) RIJKSUNIV UTRECHT.
 XX (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
 XX Pettersson-Fernholm AM, Tommassen JPM;
 XX WPI; 1999-190165/16.
 XX P-PSDB; AAW93494.
 XX New lactoferrin-binding protein B polynucleotides - obtained from
 PT Neisseria meningitidis, used to develop products for the diagnosis,
 PT prevention and treatment of neisserial disease, e.g. meningitis.
 XX Claim 2; Page 90-94; 116pp; English.
 XX This invention describes novel lactoferrin-binding protein B (LbpB)
 CC strains of Neisseria meningitidis. The products of this invention can be
 CC used for vaccinating humans against neisserial disease e.g. meningitis.
 CC Antibodies raised against the proteins of the invention can be used for
 CC diagnosing or treating neisserial disease in humans. The LbpB
 CC polypeptides can also be used for identifying compounds which inhibit the
 CC polypeptides
 XX Sequence 2226 BP; 683 A; 483 C; 571 G; 489 T; 0 U; 0 Other;
 SQ

Query Match 63.8%; Score 1442.2; DB 2; Length 2226;
 Best Local Similarity 80.3%; Pred. No. 0;
 Matches 1828; Conservative 0; Mismatches 383; Indels 56; Gaps 9;

QY 1 ATGTGTAACCGAATTATGGCGGCAATGCTGTGTTGGTCCCTTACTTTTACGATCTGTATC 60
 DB 1 ATGTGTAACCGAATTATGGCGGCAATGCTGTGTTGGTCCCTTACTTTTGGCATCTGTATT 60
 QY 61 GCGCGCAATTCGCGGTACAGCTGTGTTGCAATCAACGCGCGCGCGCACTCTGTCA 120
 DB 61 GCGCGCAATTCGCGGTACAGCTGTGTTGCAATCAACGCGCGCGCG----- 108
 QY 121 GATTCGAAATCTTCCAAATCTGCGGATAAGCTGTCTCCAGCTCTTCCGAGCCCTTCGGTA 180
 DB 109 TACCCCGTCACTTTCAAGTCTAAGGACGTTCCCACTCCGCCCCCTGCCAATCTTATA 168
 QY 181 GAAATCAGCCGGT-----CAAGCGGCGCGCGTGGTGGGCAATGCGGCTGCCAAG 234
 DB 169 GAAACCAAGCGCGGTGCGGTCAACCGGCGCTGCGGTGCGGCAATGCGGCTGTTGAG 228
 QY 235 CGGAATATCGCAACTTTTGATAAAATGGTAATCAAAATTCCTTCCATAGTAAAGAGAG 294
 DB 229 CGGATTTTCGCACTTCTGATAGGTTGGCAATGATTTTCCAAATAGCAACAAGCAGAA 288
 QY 295 GAGTATCGCGCTCAAGAGAGAGATATCTGTTTATAGACGCTAGCGCGCAAGAGACAG 354
 DB 289 GAAAAGCTGTCGTTTAAAGAGAGTGATGTTCTGTTTATACGTTTCAAAAAGATATA 348
 QY 355 GCTGACAACTTAAAGAGGAATCAAGGAGGATCTTATGACCAATCTACACCTCC 414
 DB 349 CTTCAGTGGCTTAAAGGATAAAATTCATCAACGCAATCTTATGTAGAAATTAGGACATCA 408
 QY 415 GATTTAAAGATGATGCTATCAATATAATATCTCGGCGCGATATGTTTATCTAGA 474
 DB 409 GAAATGAAATAAAATAATGGTTATGTAATTTTGGATGCGGTTATGTATATACTAAA 468
 QY 475 TATGGAACAGATGAAATCGAACAGAACTCAGCGCGGTAAAGCGGTTACCCACCGCTTAGGT 534
 DB 469 AACGGAACAGATGAAATTTAGTGGACTTCAAATCGCAAGCAGTTCCTTAATCGTTTGGC 528

QY 535 TATGACGGTTTTGTATATTTATTCGGAGAAACGTCCTTCCCAATCTTTACCGAGTCGGGA 594
 DB TACGACGGTTTTGTATATTTATTCGGAGAAACATCTTCCCAATCTTTACCGAGTCGGGA 588
 QY 595 ACGGTGGAAATATCTGGTAACTGGCAATATATGACCGATGCCAAACGTCATCGACAGGT 654
 DB ACGGTGCAATATTCGGTAACTGGCAATATATGACCGATGCCAAACGTCATCGACAGGA 648
 QY 655 CAGGC---GTTGGCATTGCAATTTGGTTATATACATTTTATGTTAAACCATGTTGTT 711
 DB AAAGCAGAGATCTTACGAGATTTGGTTATCTCGTTTATACGGTAAATATGCGGA 708
 QY 712 GCAACTTCTTATGCGGCTAAGGATGTCGACAAAGGAGAAAGCATCTTCCCAATATACG 771
 DB GCAACTTCTTATGCTGCGACTGCCGACGACCGGAGGAGAAACATCTTCCGCAATATACG 768
 QY 772 GTTGATTTTGTATAACAAACCATGATGATGCGAAGCTGATTAATAATCAGTATGTGGAAT 831
 DB GTTGATTTTGTATAACAAACCATGATGATGCGAAGCTGATTAATAATCAGTATGTGGAAT 828
 QY 832 AAAAAGATGAACCCAAAAAACCGCTGACCATTTTACGACATTTACTGCAAAATTTGACCGC 891
 DB AAAACCGATGA---AAGAACCATGACCATTTTACGACATTTACCGCAACATTTGACCGC 885
 QY 892 AACCGTTTACCGGAGTGCAGTCAATCTGATTTTACGCAAAAACCTTTCGCGGTAT 951
 DB AACCGTTTACCGGAGTGCAGTCAATCTGATTTTACGCAAAAACCTTTCGCGGTAT 945
 QY 952 GAGCGTTTGTGTTTCCATGCGGATGCGATCAGCGGCTTGAAGGCGGTTTTTTCGCGCAT 1011
 DB GAGCATTTGTTTTCATACCGATGCCGATCAGCGGCTTGAAGGCGGTTTTTTCGCGCAT 1005
 QY 1012 AACCGAGAGAGCTTTCGCGAGCTTTTATCAGCAACGACACACAGCTTTCGCGGTATTC 1071
 DB AAGCGGAGAGAGCTTTCGCGAGCTTTTATCAGCAACGACACACAGCTTTCGCGGTATTC 1065
 QY 1072 GCAGGCAAAAACACAGAGACAGCAAAACGACAGATACAAACCTTTCGCGCTCGGA 1131
 DB GCAGGCAAAAACACAAACGACATCAACGACAGATACAAATCTTGTCTATGCGCTCGGA 1125
 QY 1132 AAACACACAAATCTTGGATCTCTTAAATTTTCGTTGACGAGGCGACTGATGGCAT 1191
 DB AAACACACAAATCTTGGATCTCTTAAATTTTCGTTGACGAGGCGACTGATGGCAT 1185
 QY 1192 GCGCGTAAGTTTGCACTTCTCTATGCGGATTTTGTGTCATCCCGCAAACTTCTTGTTC 1251
 DB GCGCGCGGTTTGCACTTCTCTATGCGGATTTTGTGTCATCCCGCAAACTTCTTGTTC 1245
 QY 1252 GAAGGGCGTGAATTCCTTTTGGTAAACGAGAAACAAATCATCAAGCTTTCGCGAGGAGG 1311
 DB GAAGGGCGTGAATTCCTTTTGGTAAACGAGAAACAAATCATCAAGCTTTCGCGAGGAGG 1305
 QY 1312 AAATGACCGTCCGTGTTGTTGCGACTTTTGTACCTTATGTGAACTCTGGAACGATATAA 1371
 DB AAATGACCGTCCGTGTTGTTGCGACTTTTGTACCTTATGTGAACTCTGGAACGATATAA 1365
 QY 1372 ACCGATCCGCGGCAAGTAAACAAAGCGGAGATAAAGGAGGAGATGAGAGGTTGCA 1431
 DB ACTGACCGCGGCAAGTAAACAAAGCGGAGATAAAGGAGGAGATGAGAGGATGAGAGTACA 1425
 QY 1432 GCGGTTGATTAACGACGAAAGAAC---GAAGACGAAAGCCGTAGAAAGACGAGGCGGAA 1488
 DB GCGGTTGATTAACGACGAAAGAAC---GAAGACGAAAGCCGTAGAAAGACGAGGCGGAA 1485
 QY 1489 GAGACGAACTTCCGAGAGGATTAATGCGGAAGACGAGAGCAACCGCGAGAGAA 1548
 DB GAGACGAACTTCCGAGAGGATTAATGCGGAAGACGAGAGCAACCGCGAGAGAA 1536
 QY 1549 ACCGAGAGAGCTTATGAAGCGGAGAGGAGGATTTGAGAACCCGAGAGAAATCCCGC 1608
 DB AACGAGAGAGCTTATGAAGCGGAGAGGAGGATTTGAGAACCCGAGAGAAATCCCGC 1596

QY	660	--GTTTGGCATTGACAAATTTTGGTTTATATCA	CATTTTATGGTAAACGATGTTGGTGCAACT	7117		
Db	649	GGAGATCTCTAGCGAAGATTTGGGTTTATATCG	TTTATTACGGTCAAAA	TGTCGAGCAACT	708	
QY	718	TCATTACGGCGTTAAGGATGTCGACGAAAGGGA	AAAGCATCTCTGCCAAATATACGGTTGAT	777		
Db	709	TCATTATCTGCGACTGCGCAGCACCGGGAGGAA	AACATCTCTGCCGAATATACGGTTAAT	768		
QY	778	TTTGTATAA	CAAAACCATGAATGGCAAGCTGATTAA	AAAAATCACTATGTGCGAAATAAAAA	837	
Db	769	TTTCGACCAAAA	AACCTCTGATCGCAAGCTGATTA	AAAAATCACTATGTGC---AAAGAGA	825	
QY	838	GATGAACCCAAAAACCGCTGACCATTTACGCA	TATCTACTGCAAAATGAGCGCAACCGC	897		
Db	826	GATGATCTCTAAAAAACCACTGACCATTTACG	ACATTTACTGCAAAATGSAACCGCAACCGC	885		
QY	898	TTTTACCGGCAGTGC	CAAGGTCAATCCTGATTTAGCGAAAAAC	CTTGCGCGTATGAGCGT	957	
Db	886	TTTTACCGGCAGTGC	CAAGGTAAACA	CAGAGGTGAAGACGAATCACGCTGATAAAGATAT	945	
QY	958	TTGTTTTCCTATGCCGATGCCGATCAGCGGCT	TGAGGCGGTTTTTTTCGGCGATAAACGA	1017		
Db	946	TTGTTTTCCTATGCCGATGCCGATCAGCGGCT	TGAGGCGGTTTTTTTCGGCGATAGGGG	1005		
QY	1018	GAAGAGCTTGC	CGACGGTTATCAGCAACGACACACGCGTAT	TTCGGCGTATTCGCAAGC	1077	
Db	1006	GAAGAGCTTGC	CGACGGTTATCAGCAACGACACACGCGTAT	TTCGGCGTATTCGCAAGC	1065	
QY	1078	A---AAAAA	CAGACAGCAACGACAGATACAAACCTG	CGCTCGCTCTGGA	1134	
Db	1066	AAA	CAAAAAACAGACAGCAACGACATCAGATACA	ATCTCTGCGCTCGCTCTGGA	1125	
QY	1135	CACACCAAAATCTTGGA	TTCTCTAAAAATTTCCGTTGACGAGGCGACTGAT	GGCCATGCC	1194	
Db	1126	CACACCAAAATCTTGGA	TTCTCTAAAAATTTCCGTTGACGAGGCAAGTG	TGGAATATCC	1185	
QY	1195	CGTAAGTTTGGCAATTCCTCTATG	CCGANTTTGGTCAATCCCGACAAATCTCTTGT	CGAA	1254	
Db	1186	CGACCGTTTGAGGTTTCCACTATG	CCCGATTTTGGTCAATCCGACAAATCTCTTGT	CGAA	1245	
QY	1255	GGGCGTGAAATTCCTTTTGGTAAACGA	AGAAACAATCATCAAGCTTGC	GACGAGGAA	1314	
Db	1246	GGGCGTGAAATTCCTTTTGGTAAACAA	AGAAACAATCATCGATCTTGC	GACGAGGAA	1305	
QY	1315	ATGACCGTCCGTGCTTGTGCGACTTTT	TGACCTATGTGAACCTCGACGATAA	AAAC	1374	
Db	1306	ATGACCGTCCGTGCTTGTGCGACTTTT	TGACCTATGTGAACCTCGACGATAA	AAAC	1365	
QY	1375	GATCGCCGGCAAGTAAACCAAGCGGGA	AGATAAAGGGGAGGATGAAGGGTGCA	AGC	1434	
Db	1366	GAA	CGCCCGCTTCCAAACCGACGCGCAGGATGAAGGGGACGAAGGGTGTA	AGC	1425	
QY	1435	GTTCATAAACAGCAAGAAACG	AGACGACGACCGGTAGAACGACGAGCGCGGAAGAGAC	1494		
Db	1426	GTTCATAAACGATAAGAAAGCGA	AGACGAAATCGCGCATGAAGAAACCA	CCGAGACGA	1485	
QY	1495	GAA	ACTTCCGAAGAGGATAATGGCGGAAGACGAAGCAACCGCGCGAAGAGAAACCGCA	1554		
Db	1486	G-----TCGTAGAAGATGAAGACGAAGATGA	GA-----CGAAGAAAGATATCGAA	1530		
QY	1555	GAAGTTGATGAACCGGAAGAGAGGAAGTTGA	AGAACCCGAGAAATATCCCGCGCAGAA	1614		
Db	1531	GAAGAACTTGAAGAAAGAGCTGAAGAGGA	AGAAACCCGAGAAATATTCGCGCAGAA	1590		
QY	1615	GGCAACCGCGTTCAGCGACATCTCGCTG	CCCTAGAACGCTCTAAAGCAGGACATC	1674		
Db	1591	GGCAACCGCGTTCAGCGACATCTCGCTG	CCCTAGAACGCTCTAAAGCAGGACATC	1650		
QY	1675	GACCTTTTCTGAAGAGTATCCG	CACGGCAGAAACGGATATTCGCAAAACCGGAA	CGCG	1734	
Db	1651	GACCTTTTCTGAAGAGTATCCG	CACGGCAGGACCGACATTC	CAAAAACGGAA	CGCG	1710
QY	1735	CATTATACCGGCACTTGGGAAGCGGCTAT	CGCAAAAC-----CCATTCAA	1779		

Db	1711	CATTATACGGCACTTGGGAAGCGGTATCGCGTATCGGATAGTGTA	CGTCCATTCAA	1770
QY	1780	TGGGCAATCATGGCGGATGAAAAAGCGCAAAAGCAGAAATTACCGTGTGATTTGCACAAG	1839	
Db	1771	AAGGATAGCTATGCGAAT---	CAAGGGCAAAAGCAGAAATTACCGTGTGATTTCGAAGCG	1827
QY	1840	AAATCGATTTCCGGAAGCTGAACGGAGCAAAAACGGCGTAGAACGTGTTCCATATTGAA	1899	
Db	1828	AAGACGGTGTCCGGAATGCTGACAGAAAAAAATGATACAACCCCGCTTTTATATTGAA	1887	
QY	1900	GACGCGAAGATTGATGCGCAACGGTTTCCACGCGACAGCGCGCACTCGGAGAGCGGGATC	1959	
Db	1888	AAAGGTGTGATGTACGGTAAACGGTTTCCACGCTTTGGCGCATCTCGGAGAACGGTATT	1947	
QY	1960	AATCTTTCCGGAATGGTTGCACCGACCCCAAAACATTCCAAGCTAGTAACTCTTCGTGA	2019	
Db	1948	GACCTTTCTGGCAGGGTTTGCATNACCCGAGAACCTTCAAGCCGCAACTCTTCTTGTA	2007	
QY	2020	GAAGGAGGATTTTACGCCCGCCGAGCGCGCGGAATTCGGCGGTACTATTTTCAATAATGAT	2079	
Db	2008	ACAGCGGCTTTTATGCCCCGCGAGCGGCAGAAATTCGGCGGTAAATTAATTCGACAGCGAC	2067	
QY	2080	GGGAAATCTCTTAGTATAACTGAAATATTGAAAAATGAAGCTGAAGC	2126	
Db	2068	CGGAAATTCGGTTCGGTATTTCGGGGCGGAAAAAGATGACAAGGAGCG	2114	

RESULT 8
AAX23320

ID AAX23320 standard; cDNA; 2169 BP.

AC AAX23320;

DT 11-JUN-1999 (first entry)

DE N. meningitidis strain M981 LbpB cDNA.

LbpB; lactoferrin binding protein; vaccine; neisserial disease; meningitis; diagnosis; treatment; ds.

OS *Neisseria meningitidis*.

	Key	Location/Qualifiers
FT	CDS	1. .2169
FT		/*tag= a
FT		/product= "LbpB"

AA
PN
WO9909176-A1.

25-FEB-1999.

PF 10-AUG-1998; 98WO-EP005117.

PR 15-AUG-1997; 97GB-00017423.

FK 03-FEB-1996; 98GB-00002544.
XX

PA (TECH-) TECHNOLOGY FOUND T

PI Pettersson-Fernholm AM, Tommassen JPM:

DR WPI; 1999-190165/16.

XX
XX
FOLD, 100-1
956.

PT *Neisseria meningitidis*

PS Claim 2; Page 82-86: 116pp: English.

CC This invention describes novel lacto

cc strains of *Neisseria meningitidis*. The products of this invention can be

CC used for vaccinating humans against neisserial disease e.g. meningitis.
 CC Antibodies raised against the proteins of the invention can be used for
 CC diagnosing or treating neisserial disease in humans. The IbpB
 CC polypeptides can also be used for identifying compounds which inhibit the
 CC polypeptides

SQ Sequence 2169 BP; 675 A; 457 C; 550 G; 487 T; 0 U; 0 Other;

Query Match 55.3%; Score 1250.6; DB 2; Length 2169;

Best Local Similarity 76.9%; Pred. NO. 2.4e-298;

Matches 1641; Conservative 0; Mismatches 429; Indels 63; Gaps 7;

QY	1	ATGTGTAACCGAATTATGCGGCAATCTCTGTGTGCGCTTACTTTTAGCATCTTGATC	60
DB	1	ATGTGTAACCGAATTATGCGGCAATCTCTGTGTGCGCTTACTTTTAGCATCTTGATC	60
QY	61	GCGGCAATTTTCGGGTACAGCTGTGTGCAATCAACGCGGACGCGCAACTCTGTCA	120
DB	61	GCGGCAATTTTCGGGTACAGCTGTGTGCAATCAACGCGGACGCGG-----	108
QY	121	GATTCGAATCTTCAATCTCGGATAGCTGTCTCAGCTCTCTGCGAGCTTCGGTA	180
DB	109	TACCCGTCACCTTCAAGCTTAAGGACGTTCCCACTTCGCCCCCTGCGGGTCTTCGGTA	168
QY	181	GAAATCACCGGTCGCAAGCGCCCGCTCGGTGCGCAATCGGCTGCCAAGCGGAAT	240
DB	169	GAAACACCGCGGTCAACAGCCCGCGCTCGGTGCGCAATCGGCTGTGAGACGGAAT	228
QY	241	ATCGCAACTTTTGATAAATAATGTAATGAAATTTCCCAATPAGCAGCGAGAGAT	300
DB	229	ACTGCTTTTCATCGTAGATGGCAGCGCAATTCGCGATAGCAACAAGCAAGAAAG	288
QY	301	CTGCGCTCAAGAGAGGATATCTCTGTTTATAGAGGTACCGGAAAGACAGCTGAC	360
DB	289	CTGCTGTTTAAAGAGGTGATCTCTGTTTATATACGTTTCAAAAGAAATAAATCTCA	348
QY	361	AAACTTAAAGGAATCAACGCGGATCTTAATGACCAATCTACAGCTCCGATTTA	420
DB	349	CACTTAAAGCGAATTCATAAGTAATCTGAGGACGATTAACCATCGGAAT	408
QY	421	AAAGATGATGCGTATCAATATAAATATGTCCGGGCGGATATGTTTATCTAGATATGA	480
DB	409	GAAATATAAATAATAATATATCGGTTTGTCTAGTCCGGTTATGTGTTTACTAAACGGA	468
QY	481	ACAGATGAATTCGAACAGACTCAGCGGTAGCGGTTTACCCACGCTTAGTTATGAC	540
DB	469	AAAGATGAATTTGAGAAACATCGGATGAAAGAGTCTTCTAATCGTTTAGGCTATGAC	528
QY	541	GGTTTGTATATATTTCGGGAAACGTCCTTCCCAATCTTTACCGAGTCCGGAAACGGTG	600
DB	529	GGTTTGTATATATCTCGAGAAACATCTTCCCAATCTTTACCGAGCGGGAGCGGTG	588
QY	601	GAAATATCTGTGTAACGCAATATATGACCGATGCAACGTCATCGACAGGTGAGGG	660
DB	589	AAATATTCGCGCAACTGGCAATATATGACCGATGCCATACGTCATCGAGAGGTAGGGG	648
QY	661	GTTGCGATTGCAATTTGGGTTATATCACTTTATGTTAGTAAAGTGTGGTGCACTTCT	720
DB	649	GTTTCAGTGTGGATTGGGTTATACCATATATATGTTGTAATGAAATTTGGGAGCTTCT	708
QY	721	TATGCGGTAAAGATTCGACGAAAGGAAAGCATCTCGCAAAATATACGGTTGATTTT	780
DB	709	TATGAGCTAGGATGCGGATGCGCGGAAACATCTCTGCGCAATATACGGTTAATTC	768
QY	781	GATAACAAACCAATGAATGGCAAGCTGATTAATAAATCAGTATGTGCGAATAAAGAT	840
DB	769	GACAAAAAACCCTGAAGTAAGTTGATTAATAAATCAGTATGTC---AAAAAGAGAT	825
QY	841	GAACCCAAAAACCGCTGACATTTACGACATTTACTGCAAAATTTGACGCGCAACCGCTT	900
DB	826	GATCCTAAAAATCCATGACATTTTAAACATTTACCGCAACATTTGACGCGCAACCGCTT	885
QY	901	ACCGGAGTCCCAAGTCAATCTGATTTAGCGAAAAACCTTCCCGGTATGAGCGCTTG	960

DB	886	ACCGGAGTGCAGAGTTAGCACCGAGGTGAAGACGCAACACGCTGATAAAGAAATTTTG	945
QY	961	TTTTTCATGCGGATGCGGATCAGCGCTTGAAGCGGTTTTTTTCGGGATTAACGAGAA	1020
DB	946	TTTTTCATGCGGATGCGGATCAGCGCTTGAAGCGGTTTTTTTCGGGATTAACGAGAA	1005
QY	1021	GAGCTTCCGAGCGGTTTATCAGCAACGCAACAGCGTATTTTCGGGATTTCCGAGGCA--	1078
DB	1006	GAGCTTCCGCGCGGTTTATCAGTAAACGCAACAGCGTATTTTCGGGATTTCCGAGGCA	1065
QY	1079	AAAAAACAAGACAGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCA	1137
DB	1066	CAAAAAACAAGACAGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCA	1125
QY	1138	ACCAAAATCTTGGATCTCTAAATAATTTCCGTTGACGAGGCGACTGATGGCCATGCCGT	1197
DB	1126	ACCAAAATCTTGGATCTCTAAATAATTTCCGTTGACGAGGCGACTGATGGCCATGCCGT	1185
QY	1198	AAGTTTGCATTTCTCTATGCGCGATTTTGGTTCATCCGACAAATCTTTTTCGAGGG	1257
DB	1186	AAGTTTGCATTTCTCTATGCGCGATTTTGGTTCATCCGACAAATCTTTTTCGAGGG	1245
QY	1258	CGTGAATTCCTTTGGTAAACGAAACAAATCATCAAGCTTCCGACGCGCAGGAAATG	1317
DB	1246	CGTGAATTCCTTTGGTAAACGAAACAAATCATCAAGCTTCCGACGCGCAGGAAATG	1305
QY	1318	ACCGTCCGCTGCTTGTGCGACTTTTGTGACCTATGTGAAATCTCGGACGATAAAAACCGAT	1377
DB	1306	ACCATCCGCTGCTTGTGCGATTTTCTGACCTATGTGAAATCTCGGACGATAAAAACCGAC	1365
QY	1378	CGCCCGGCAAGTAAACCAAGCGGAGATTAAGGGGAGGATGAAGAGGTCAGCGCTT	1437
DB	1366	CGCCCGCGCTCAACCGAAGCGGACGATGAAGAGGATTCGACATTTGATTAATGCGGAA	1425
QY	1438	GATAACGACGAAAGAAA---GCGAAGACGAGCCGTAGAAGACGAGCGCGGCAAGAGAC	1494
DB	1426	GAAAGCGAAGACGAAATTTCCGAGATGATACGCGGAGATGAAGTCAACCGAAGAGAG	1485
QY	1495	GAAACT-----TCCGAGAGGATTAAGCGGAGACGAGGACGACCCCGCAAGAGAA	1548
DB	1486	GAACTGAAAGAACGAAAGAGAAATCTGATGAAGACGAGAGAGAGAACCCCGAAGAACT	1545
QY	1549	ACCGAAGAGTGTGATGAAGCCGAGAGGAGGAGTGAAGAACCCCGCAAGAGAAATTCGCG	1608
DB	1546	GAAAGAACTGAAGAAACTGAAGAACTGAAGAACTGAAGAACTGAAGAAATTCGCG	1605
QY	1609	---GCGAAGGCAACGCGGTTTTCAGCGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	1665
DB	1606	ACGAAAGAGGCAACGCGGTTTTCAGCGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	1665
QY	1666	AGGACATCGACCTTTCTGAAAGGTATCCGACGCGGAGGAGGATTTCCGCAAGC	1725
DB	1666	AGGACATCGACCTTTCTGAAAGGTATCCGACGCGGAGGAGGATTTCCGCAAGT	1725
QY	1726	GGAAGCGGCTATTATACCGGCACTTTGGGAGGCGGTATCGGCAAAACCCATTTCAATGGGAC	1785
DB	1726	GGAAGCGGCTATTATACCGGCACTTTGGGAGGCGGTATCGGCGTCCGCGATGAAGAGG	1785
QY	1786	AATCAGCGCGGTG-----AAAAAGGCAAAA	1812
DB	1786	GAAACGCTAGATGGCACTACGTCCTCAATTTCAAAGGATAGTATGCGAATCAAGCGGCAAA	1845
QY	1813	GCAGAAATTTACCGTTGATTTTCGACAAAGAAATCGATTTCCGAAAGCTGACGAGGCAAAAC	1872
DB	1846	GCAGAAATTTGACGTTGATTTTGTGCGAAGTCTGCTTTTCAAGTGAAGTTGACAGAAAT	1905
QY	1873	GGCGTAGAACCTGCTTTTCCATATTGAAGACGCGCAAGATTTGATGGCAACCGTTTCCGCG	1932
DB	1906	GATACACACCCGCTTTTATATTTGAAAAGGTTGATTTGATGGCAACCGTTTCCGCT	1965
QY	1933	ACAGCGGCTCTCGGAGAGCGGATCAATCTTTTCGGGAAATGTTTCGCGGACCCCAAA	1992

Db 1966 TTGGCGGCTACTCGTGAATAATGGTGTGATTTGTCTGGCGCAGGTTGACATAATCCCAA 2025
 QY 1993 ACATTCGAAGCTAGTAATCTTCGTGTAGAGGAGGATTTTACGGCCCGCAGCGCGCGGAA 2052
 Db 2026 AGTTTAAAGCGCAGTAATCTTCGTGTAGAGGAGGATTTTATGGTCCGCGCGCGCAGAG 2085
 QY 2053 TTGGCGGCTACTATTTCATTAATAATGATCGGAAA 2085
 Db 2086 TTGGGTGTAATATATATATGACAGTGACCGGAAA 2118

RESULT 9
 AAA81482/C
 ID AAA81482 standard; DNA; 14652 BP.
 AC AAA81482;
 XX
 XX 04-DEC-2000 (first entry)
 XX N. meningitidis partial DNA sequence gnm_30 SEQ ID NO:30.
 DE Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 XX antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; MenB; ds.
 XX Neisseria meningitidis.
 OS
 XX
 XX W0200022430-A2.
 XX
 XX 20-APR-2000.
 XX
 XX 08-OCT-1999; 99WO-US023573.
 XX
 XX 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 PI Rappuoli R, Pizza M;
 XX
 XX WPI; 2000-318079/27.
 XX
 XX Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.
 XX
 XX Claim 7; Page 582-586; 1760pp; English.
 XX
 XX The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not

CC antigenically variable or at least more conserved than other more
 CC variable regions
 XX
 SQ Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;
 Query Match 48.6%; Score 1100.2; DB 3; Length 14652;
 Best Local Similarity 85.3%; Pred. No. 7e-261;
 Matches 1334; Conservative 0; Mismatches 163; Indels 66; Gaps 7;
 QY 712 GCAACTTCTTATGCGGCTTAAGGATGTCACAAAGGAAAAAGCATCTTCGCAAAATATACG 771
 Db 14652 GCAACTTCTTATGAGGCTAGGATGCCAGCAGGGAAGCAATCTTCGCAATATACG 14593
 QY 772 GTTGATTTTGATAACAAAAACCATCAATGGCAAGCTGATTAATAAATCAATGTGCAAAAT 831
 Db 14592 GTTGATTTTGATAACAAAAACCATCAATGGCAAGCTGATTAATAAATCAATGTGCAAAAT 14533
 QY 832 AAAA-----AAGATGAACCCAAAAACCGCTGACCATTTACGACATTTACGCAAAATG 885
 Db 14532 AAAAGTAATCCAAATGAGCCCAAAAAACCGCTGACCATTTACGACATTTACGCAAAATG 14473
 QY 886 GACGCCAACCGCTTTACCGGCAGTGCCAAAGTCAATCTGATTTAGCGAAAAAATCTGCC 945
 Db 14472 GACGCCAACCGCTTTACCGGCAGTGCCAAAGTCAATCTGATTTAGCGAAAAAATCTGCC 14413
 QY 946 GGTAAATGAGCGTTTGTGTTTTCATGCCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTC 1005
 Db 14412 GATAAAGATATTTGTTTTCATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTC 14353
 QY 1006 GCGGATAACGAGAGAGCTTGCGGAGCGGTTTATCAGCAACGACCAACAGCGGTATTCGGC 1065
 Db 14352 GCGGATAACGAGAGAGCTTGCGGAGCGGTTTATCAGCAACGACCAACAGCGGTATTCGGC 14293
 QY 1066 GTATTTCGAGGCA-----AAAAAACAAGACAGCAAAACGACAGATACAAAACCTGCCCTG 1122
 Db 14292 GTATTTCGAGGCAACCAAAACAAGACAGCAAAACGACAGATACAAAACCTGCCCTG 14233
 QY 1123 CCGTCTGGAAAAACACACCAAAATCTTGATTTCTTAAAAATTTCCGTGACGAGCGGACT 1182
 Db 14232 TCGTCTGGAAAAACACACCAAAATCTTGATTTCTTAAAAATTTCCGTGACGAGCGGACT 14173
 QY 1183 GATGCCCATGCCGTAGTTTGGCAATTTCTCTATGCCCGATTTTGTCTATCCCGCAAAA 1242
 Db 14172 GATAAAATCCCGGTAGTTTGGCAATTTCTCTATGCCCGATTTTGTCTATCCCGCAAAA 14113
 QY 1243 CTCTCTGCAAGGCGGTGAAATTTCTTGTGTAACGAAAGCAAAATCATCAAGCTTGCC 1302
 Db 14112 CTCTCTGCAAGGCGGTGAAATTTCTTGTGTAACGAAAGCAAAATCATCAAGCTTGCC 14053
 QY 1303 GACGCGAAGAAATGACCGTCCGTGTTGTTGGACTTTTGTGACCTATGTGAAACTCGGA 1362
 Db 14052 GATGTTAGGAAAAACGACAAATCCGAAACCTGCTGCGATTTTCTGACCTATGTGAAATCGGA 13993
 QY 1363 CGGATAAAACCGCATGCCCGGCAAGTAAACCAAGCGGCAAGATTAAGGAGGAGTGA 1422
 Db 13992 CGGATGCAAAACCGCATGCCCGGCAAGTAAACCAAGCGGCAAGATTAAGGAGGAGTGA 13933
 QY 1423 GAGGTTGACGCGCTTGTATACGACGAAAGGCAAGACGAAACCGTAGAAGACGAGGC 1482
 Db 13932 GAGGATAACGCGCTTGTATACGCTCGAAGAGGCGAAGACGAAATCGAGATGAAGAGGC 13873
 QY 1483 GGCAGAGAGACGAAACTTTCCGAAAGAGGTAATTTGGCGAAGACGAAAGCAACCGCGGAA 1542
 Db 13872 ACCGGAAGCG-----CAGCGGTAAAAACGAAAGGACGAGGAA 13834
 QY 1543 GAGGAAACGAGAGAGTTGATGAGCGGAGAGGAGGAGTTCGAAACCGGAGGAA 1602
 Db 13833 GAGGAAACGCGTAGAGGT-----GAGAGTGAAGCTGAAGAACCGGAGGAA 13786
 QY 1603 TCGCCCG---GCAGAGGCGAACCGCGGTTCAGGCGAGCATCTGCTGCCCTTAGAGGCTCT 1659
 Db 13785 TCGCCCGCAGAGAGAGCGGCGAGCGGTTTCAAGCGGATCTCTGCCCGCTCCGGAAGCCCT 13726

QY 1660 AAGGACGAGCATCGACCTTTCTGAAAGGTATCCGCGCAGAAACGGATATTCGG 1719
 Db |||||
 QY 1720 CAAGCGGAAACGGCGCATATACCGGCACTTTGGGAAGCGGTATCGGCAAAACCCATTCAA 1779
 Db |||||
 QY 1780 TGGGACAAATCAGCGCGATGAAAGAGCGGCAAAACAGAAATTTACGTTGATTTGCACAG 1839
 Db |||||
 QY 1840 AATTCGATTTCCGGAAGCTGACGAGCAGCAACGCGGTAGAACCTGCTTCCATATTGAA 1899
 Db |||||
 QY 1900 GACGCGAAGATTTGATGCAACGCTTTCCACGCGACGCGCACTCGGGAGAGCGGCAATC 1959
 Db |||||
 QY 1960 AATCTTTCCGGAATGTTGACCGACCGCAACCCAAACATTCAGCTAGTAATCTTCGTGTA 2019
 Db |||||
 QY 2020 GAAGGAGATTTTACGCGCGCGCGCGGCAATTTGGCGGTACTATTTCATAAATGAT 2079
 Db |||||
 QY 2080 GGGAAATCTCTTGTATATACTGAAATATTTGAAATGAAGCTGAAGTTGAAATT 2139
 Db |||||
 QY 2140 GAAGCTGAGCTGAGTGAAGTTGAGCTGATGCTGCAACAGTTAGACCTGATGAA 2199
 Db |||||
 QY 2200 GTTAAACACAAATTCGGCGTGGTATTCGGTCCGAAAGAAATATGCGAGAGGTGAAAAA 2259
 Db |||||
 QY 2260 TGA 2262
 Db |||||
 QY 2306 GTTAAACACAAATTCGGCGTGGTATTCGGTCCGAAAGAAATATGCGAGAGGTGAAAAA 13147

RESULT 10
 AAF91389
 ID AAF91389 standard; DNA; 1000 BP.
 XX
 AC AAF91389;
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE N. meningitidis (serogroup B) LbpA gene upstream sequence, SEQ ID:15.
 XX
 KW Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine;
 KW genetically modified; protective antigen expression; LPS detoxification;
 KW LPS; lipid A; homologous recombination vector; immunisation;
 KW immunoprotective; non-toxic; paediatric; cyclic; circular; ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200109350-A2.
 XX
 PD 08-FEB-2001.
 XX
 PF 31-JUL-2000; 2000WO-EP007424.
 XX
 PR 03-AUG-1999; 99GB-00018319.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Berthet FU, Dalemans WLJ, Denoel P, Dequesne G, Feron C, Lobet Y;

PI Poolman J, Thiry G, Thonnard J, Voet P;
 XX WPI; 2001-138654/14.
 XX
 PT New isolated polynucleotide useful for outer membrane vesicle preparation
 PT from Gram-negative bacterial strain for vaccination of microbial
 PT infections.
 XX
 PS Claim 46; Page 81; 120pp; English.
 XX
 CC The invention relates to a genetically-engineered outer membrane vesicle
 CC (bleb) preparation from a Gram-negative bacterium for use as a vaccine.
 CC The blebs of the invention are improved with respect to their
 CC immunogenicity and toxicity by the introduction of one or more genetic
 CC changes to the chromosome of the bacterium from which the blebs are
 CC derived. The changes made include the upregulation of protective antigen
 CC expression, the downregulation of immunodominant non-protective antigen
 CC expression, and genetic changes which result in detoxification of the
 CC Lipid A moiety of lipopolysaccharide (LPS). The invention also
 CC encompasses modified Gram-negative bacterial strains from which the bleb
 CC preparations are made, a vector suitable for performing recombination
 CC events (for the generation of the modified bacterial strains),
 CC bacterially-derived nucleic acid sequences used in such a vector, and an
 CC immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole
 CC cell vaccine suitable for paediatric use. The bleb preparation is useful
 CC in the manufacture of a medicament for immunising a human host against a
 CC disease caused by infection of one or more of the following: Neisseria
 CC meningitidis, Neisseria gonorrhoeae, Haemophilus influenza, Moraxella
 CC catarrhalis, Pseudomonas aeruginosa, Chlamydia trachomatis, and Chlamydia
 CC pneumoniae. The invention may also be used to provide immunisation against
 CC the influenza virus. Bacterially derived nucleotide sequences of the
 CC invention are used in the performance of homologous recombination events
 CC up to 1000 bp upstream of a bacterial chromosomal gene in order to either
 CC increase or decrease expression of that gene. Immunoprotective and non-
 CC toxic Gram-negative bleb, ghost, or killed whole cell vaccines are and
 CC immunogenic, less toxic and safer, and are particularly useful for
 CC paediatric use. The present sequence represents a specifically claimed
 CC Neisseria meningitidis nucleic acid sequence
 XX
 SQ Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;
 Query Match 32.3%; Score 730; DB 4; Length 1000;
 Best Local Similarity 84.8%; Pred. No. 6.4e-170;
 Matches 882; Conservative 0; Mismatches 115; Indels 43; Gaps 4;
 QY 1222 GATTTTGGTCTATCCGACAAACTTCTTGTGCAAGGGGTGAATTCCTTTGTTAAACGAA 1281
 Db 1 GATTTTGGTCTATCCGACAAAGCTTCTTGTGCAAGGGGTGAATTCCTTTGTTAGCCAA 60
 QY 1282 GAACAAATCATCAAGCTTGGCGACGAGGAAATGACCGTCCGTGCTTGTGGACATTT 1341
 Db 61 GAGAAACCATCAAGCTTGGCGATGGCAGGAATGACCGTCCGTGCTTGTGGACATTT 120
 QY 1342 TTGACCTATGTGAACCTCGGACGATATAAAACCGATGCCCGCAAGTAACCTAAAGCG 1401
 Db 121 TTGACCTATGTGAACCTCGGACGATATAAAACCGACCGCGCAAGTAACCTAAAGCG 180
 QY 1402 GAAGTAAAGGGAGGATGAGAGGTCGAGCGCTTGTATACGACGAGAAAGGAGGAGAC 1461
 Db 181 GAAGTAAAGGGAGGATGAGAGGTCGAGCGCTTGTATACGTCGAGAGAGGCGAAGGC 240
 QY 1462 GAAGCGGTAGAAAGACGAAGCGCGGCAAGAACGAAACTTCGGAAGAGGATAATGGCGAA 1521
 Db 241 GAAGTTCCGAGATGAGCGGAGAGAGCGCAAGAAATCGTCGAGAGAA----- 290
 QY 1522 GACGAAGAGCAACCGCGGAGAGAGAAACCGAAGATTGATGAAGCCGAGAGAGAGAA 1581
 Db 291 -----ACCGAAGAGAGAAAGCTGAAGAGGAGAGAGCTGAACCCCAAGAA 333
 QY 1582 GTTGAAGAACCCGAGAGAAATATCCCGCGCAGAAG---GCAACGGCGGTTTCAGGAGCATC 1638
 Db 334 GTTGAAGAACCCGAGAGAAATATCCCGCGAGAGAGAGCGGCTTCAACGCCATC 393

Db 529 CCGGAGAACGTCCTCCCAATCTTACCGAGCGGGAAAGGTGCATATTCGGTAACT 588
 QY 617 GCGAATATATGACCGATGCCAAAGCTCATCGAGAGTCAAGCGGTGGCAATTCACAAT 676
 Db 589 GCGAATATATGACCGATGCCAAAGCTCATCGAGAGTCAAGCGGTGGCAATTCACAAT 648
 QY 677 TGGGTTATATACATATTTATGTTAAGCATGTTGGTGCACCTTCTTATGCGGCTTAAGAT 735
 Db 649 TGGGTTATACCATATATGTTAAGCATGTTGGTGCACCTTCTTATGAGGCTTAGGAT 707

RESULT 13

ID ABS67377 standard; DNA; 3300 BP.

AC ABS67377;

DT 29-NOV-2002 (first entry)

DE Neisseria gonorrhoeae lbpA gene.

DE Gram-negative bacterial bleb; PorB; outer membrane protein;

KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;

KW protective antigen; antibacterial; vaccine; gene; ds.

XX Neisseria gonorrhoeae.

OS WO200262380-A2.

PN 15-AUG-2002.

PD 08-FEB-2002; 2002WO-EP001356.

PF 08-FEB-2001; 2001GB-00003169.

PR (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

PA Berthet FU, Lobet Y, Poolman J, Verlant VGCL;

PI WPI; 2002-657510/70.

DR P-PSDB; ABG31056.

XX Novel gram-negative bacterial bleb presenting on its surface PorB outer

PT membrane protein from Chlamydia trachomatis or protective antigen from

PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.

XX Disclosure; Page 48-49; 75pp; English.

XX The present invention relates to a new gram-negative bacterial bleb

CC presenting on its surface the PorB outer membrane protein from Chlamydia

CC trachomatis, or a protective antigen from C. pneumoniae. The invention is

CC useful for preventing C. trachomatis or C. pneumoniae infection in a

CC host. The present nucleic acid sequence represents a Neisseria

CC gonorrhoeae gene as described in the invention

XX SQ Sequence 3300 BP; 897 A; 807 C; 921 G; 675 T; 0 U; 0 Other;

Query Match 7.5%; Score 169.2; DB 6; Length 3300;

Best Local Similarity 77.5%; Pred. No. 3.1e-31;

Matches 248; Conservative 0; Mismatches 33; Indels 39; Gaps 2;

QY 1943 CTCGGAGAGCGGCATCAATCTTCGGGAATGTTTCAGCGGCGGCGGATTCGGCGGTA 2062

Db 1 CTCGGATACCGCATCAATCTTCGGGAATGTTTCAGCGGCGGCGGATTCGGCGGTA 60

QY 2003 CTAGTAATCTTCGTAGAGGAGGATTTTACGCGCGGAGCGGCGGATTCGGCGGTA 2062

Db 61 CCGACAATCTCTGTACCGGCGGCTTTTACGCGCGGAGCGGCGGATTCGGCGGTA 120

QY 2063 CTATTTTCAATATGATGGGAATCTCTTAGTATAACTGAAAATATTGAAATGAAGCTG 2122

Db 121 CTATTTTCAATAGGATGGGAATCTCTTAGTATAACTGAAATATTGAAATGAAGCTG 172

QY 2123 AAGCTGAAGTTGAAGTTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 2182
 Db 173 -----TGAAGTTGAAATGAAGCTGAAGTTGCGGAAAC 204
 QY 2183 AGTTAGAACTGATGAAGTTAAACACAAATTCGCGCTGGTATTTCGGTGCCGAAGAAGATA 2242
 Db 205 AGTTAGAACCC---TGAAGTTAAACCCCAATTCGCGCTGGTATTTCGGTGCCGAAGAAGATA 261
 QY 2243 TGCAGGAGGTGGAATAATCA 2262
 Db 262 ATAAAGAGGTGGAATAATCA 281

RESULT 14

AAS68580

ID AAS68580 standard; cDNA; 963 BP.

XX AAS68580;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #4384.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US008631.

PF 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

PA Drmanac RT, Liu C, Tang YT;

PI WPI; 2001-639362/73.

DR P-PSDB; ABG04393.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX Claim 1; SEQ ID NO 4384; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic

CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences

XX Sequence 963 BP; 353 A; 171 C; 268 G; 169 T; 0 U; 2 Other;
SQ
Query Match 4.5%; Score 102; DB 5; Length 963;
Best Local Similarity 58.4%; Pred. No. 7.5e-15;
Matches 177; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
QY 1383 GGCAGTAAACCAAGCGGGAAGATAAAGGGGAGGATGAAGAGGTGAGCGCTTGATAA 1442
DB 120 GGAGAGGAAGAAGAGGAAGAAGAGGAAGAAGAGGAAGAAGAGGAAGAAGAAGA 179
QY 1443 CGACGAGAGCGGAGGAGGAGCGGTAGAGAGCGGCGGAGAGGAGCGAACTTC 1502
DB 180 AGAAGA 239
QY 1503 CGAAGAGGATTAATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1562
DB 240 GGAAGA 299
QY 1563 TGAAGCCGAG 1622
DB 300 AGAAGA 359
QY 1623 CGGTTGAGGAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1682
DB 360 CAGGACCAAGATAGACCTGGAGGATCCAGAGCTGGCCAGTTATCAGGTCTGCTGTT 419
QY 1683 CCT 1685
DB 420 CCT 422

RESULT 15
AAS75460
ID AAS75460 standard; cDNA; 400 BP.
XX AAS75460;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #11264.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX Food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US0008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG11273.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 11264; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 400 BP; 215 A; 34 C; 131 G; 19 T; 0 U; 1 Other;
Query Match 4.4%; Score 99.2; DB 5; Length 400;
Best Local Similarity 59.4%; Pred. No. 2.6e-14;
Matches 167; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
QY 1383 GGCAGTAAACCAAGCGGGAAGATAAAGGGGAGGATGAAGAGGTGAGCGCTTGATAA 1442
DB 120 GGAGAGGAAGAAGAGGAAGAAGAGGAAGAAGAGGAAGAAGAGGAAGAAGAAGA 179
QY 1443 CGACGAGAGCGGAGAGAGAGAGCGGTAGAGAGCGGCGGAGAGAGCGAACTTC 1502
DB 180 AGAAGA 239
QY 1503 CGAAGAGGATTAATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1562
DB 240 GGAAGAGGA 299
QY 1563 TGAAGCCGAG 1622
DB 300 AGAAGA 359
QY 1623 CGGTTGAGGAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAAAG 1663
DB 360 CAGGACCAAGATAGACCTGGAGGATCCAGAGCTGGCCAGTGGCCCAAG 400

Search completed: August 24, 2004, 14:38:28
Job time : 777.365 secs

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 12:38:10 ; Search time 164.35 Seconds
(without alignments)
7637.968 Million cell updates/sec

Title: US-10-735-098-7
Perfect score: 2262
Sequence: 1 atgtgtaaacgaattatgg.....tcgaggagggtggaataatga 2262

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	90.6	4.0	7218	1	US-08-232-463-14
C 2	86.2	3.8	929	4	US-09-671-317-14
C 3	86.2	3.8	1001	4	US-09-671-317-439
C 4	84.6	3.7	43795	3	US-08-742-185-101
C 5	83.6	3.7	3211	2	US-08-574-959A-8
C 6	83.6	3.7	3211	3	US-09-357-014-8
C 7	83.6	3.7	3901	2	US-08-574-959A-6
C 8	83.6	3.7	3901	3	US-09-357-014-6
C 9	77.6	3.4	390	3	US-09-197-649-7
C 10	77.4	3.4	2230	3	US-08-448-194-7
C 11	77.4	3.4	2230	4	US-08-867-921-7
C 12	73.6	3.3	3489	2	US-08-728-323A-1
C 13	73.6	3.3	3489	4	US-09-298-568-1
C 14	73.6	3.3	3489	4	US-08-410-399-1
C 15	73.6	3.3	32207	2	US-08-770-379-20
C 16	73.6	3.3	32207	3	US-08-757-669A-20
C 17	73.6	3.3	32207	4	US-09-230-371A-20
C 18	70.8	3.1	966	2	US-08-766-738-2
C 19	70.8	3.1	966	4	US-09-282-610-2
C 20	70.4	3.1	1276	3	US-09-177-325-2
C 21	70.4	3.1	1276	3	US-09-411-812A-2
C 22	70.4	3.1	1276	4	US-09-590-113-2
C 23	70.2	3.1	1277	1	US-08-676-967-2
C 24	70.2	3.1	1277	1	US-08-676-974-2
C 25	70.2	3.1	1277	2	US-09-098-487-2
C 26	67.6	3.0	58909	4	US-09-596-002-30
C 27	67	3.0	1584	1	US-07-667-276A-1

C 28	66.4	2.9	16442	3	US-08-781-891-208
C 29	66.4	2.9	16442	4	US-09-618-166-208
C 30	65.8	2.9	2223	1	US-08-257-073-4
C 31	65	2.9	696	3	US-09-461-697-193
C 32	65	2.9	699	3	US-09-461-697-191
C 33	65	2.9	717	3	US-09-461-697-189
C 34	65	2.9	774	3	US-09-461-697-187
C 35	65	2.9	819	3	US-09-461-697-185
C 36	65	2.9	1669	3	US-09-461-697-184
C 37	64.6	2.9	2518	3	US-09-433-699-3
C 38	64.4	2.8	243	1	US-08-182-175A-56
C 39	64.4	2.8	243	1	US-08-474-633A-74
C 40	64.4	2.8	243	4	US-08-823-771-74
C 41	64.4	2.8	243	5	PCT-US92-06412-56
C 42	63.2	2.8	7295	2	US-08-487-826B-15
C 43	63	2.8	2295	1	US-08-375-300-3
C 44	63	2.8	2295	3	US-09-177-431-3
C 45	63	2.8	2295	5	PCT-US95-16930-3

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Hardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
; US-08-232-463-14

Query Match 4.0%; Score 90.6; DB 1; Length 7218;

NAME/KEY: primer_bind
LOCATION: 139..158
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 634..652
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc binding
LOCATION: 489..513
OTHER INFORMATION: 12-454-363 potential probe
NAME/KEY: misc feature
LOCATION: 674..679,881..882,892..893
OTHER INFORMATION: n=a, g, c or t
US-09-671-317-14

Query Match 3.8%; Score 86.2; DB 4; Length 929;
Best Local Similarity 64.8%; Pred. No. 7,8e-13;
Matches 138; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

QY 1391 AACCAAGCGCGAAGATAAAGGGGAGGATGAAGAGGGTGCAGCGCTTGTATACGACGAG 1450
Db 878 ATCTCAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 819
QY 1451 AAAGCGAAGCAACCGCTAGAGAGGAGGCGGCGAAGAACGCAAACTTCCGAGAGG 1510
Db 818 AAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 759
QY 1511 ATAATGGCGAAGCAAGAAAGCAA-CCGCGGAGAGAAACCGCAAGAAAGAAAGAAAGCC 1569
Db 758 AAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 699
QY 1570 GAAGAGGAGGAGTTGAAGAACCCGCAAGAAAAA 1602
Db 698 GAAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 666

RESULT 3

US-09-671-317-439/c
Sequence 439, Application US/09671317
Patent No. 6528260

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

APPLICANT: Bougueleret, Lydie

APPLICANT: Cohen, Annick

TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

FILE REFERENCE: 62.US3.CIP

CURRENT APPLICATION NUMBER: US/09/671,317

CURRENT FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 09/536,178

PRIOR FILING DATE: 2000-03-23

PRIOR APPLICATION NUMBER: PCT/IB00/00403

PRIOR FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: US 60/126,269

PRIOR FILING DATE: 1999-03-25

PRIOR APPLICATION NUMBER: US 60/131,961

PRIOR FILING DATE: 1999-04-30

NUMBER OF SEQ ID NOS: 977

SOFTWARE: Patent.pm

SEQ ID NO 439

LENGTH: 1001

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: allele

LOCATION: 501

OTHER INFORMATION: 12-454-242 : deletion AT

NAME/KEY: misc binding

LOCATION: 481..500

OTHER INFORMATION: 12-454-242.misl, potential

NAME/KEY: primer_bind

LOCATION: 260..279

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer_bind

Best Local Similarity 9.6%; Pred. No. 1.4e-13;
Matches 45; Conservative 251; Mismatches 175; Indels 0; Gaps 0;

QY 1272 GGTAAACGAGAAACAATCATCAAGCTTCGCGAGGAGGAAATGACCGTCGCTGTTG 1331
Db 1430 RRR 1371
QY 1332 TTGGGACTTTTGACCTATGTGAAACTCGGACGGATATAAACCCGATCCCGCGCAAGTAA 1391
Db 1370 RRR 1311
QY 1392 ACCAAAGCGGAGAAATAAAGGGAGGATGAAGAGGTCGAGCGTTGATAACGACGAAGA 1451
Db 1310 RRR 1251
QY 1452 AAGCGAAGCAAGCCGTAGAGAGGCGGCGAAGAAAGCAAGAACTTCCGAGAGGA 1511
Db 1250 RRR 1191
QY 1512 TAATGGCGAAGCAAGCAACCCGCGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1571
Db 1190 RRR 1131
QY 1572 AGAGAGGAGGAGTTGAAGAACCCGCGAAGAAATAAGCGCGGAGGCAAGCGGCTTCAGG 1631
Db 1130 RRR 1071
QY 1632 CAGCATCTGCTGCTGCTAGAGCCTCTAAAGCGAGGAGCATCGACCTTTTCTGTGAAGG 1691
Db 1070 RRRATCGCAAGTCCCTCGACTGAGCCAGCTCGAATTAATCTGTGAGCGTATGG 1011
QY 1692 TATCCCGACGCGAGAAACGGATATCCGCAAGCGGAGCGGCATTTATAC 1742
Db 1010 CAAACGAGGAAATAAGTTATAGTAGCCGCACTCGATGGGACATTTCAAC 960

RESULT 2

US-09-671-317-14/c
Sequence 14, Application US/09671317
Patent No. 6528260

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

APPLICANT: Bougueleret, Lydie

APPLICANT: Cohen, Annick

TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

FILE REFERENCE: 62.US3.CIP

CURRENT APPLICATION NUMBER: US/09/671,317

CURRENT FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 09/536,178

PRIOR FILING DATE: 2000-03-23

PRIOR APPLICATION NUMBER: PCT/IB00/00403

PRIOR FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: US 60/126,269

PRIOR FILING DATE: 1999-03-25

PRIOR APPLICATION NUMBER: US 60/131,961

PRIOR FILING DATE: 1999-04-30

NUMBER OF SEQ ID NOS: 977

SOFTWARE: Patent.pm

SEQ ID NO 14

LENGTH: 929

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: allele

LOCATION: 501

OTHER INFORMATION: 12-454-363 : polymorphic base A or G

NAME/KEY: misc binding

LOCATION: 481..500

OTHER INFORMATION: 12-454-363.misl, potential

NAME/KEY: misc binding

LOCATION: 502..521

OTHER INFORMATION: 12-454-363.misl2, potential complement

; LOCATION: 755..773
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc feature
; LOCATION: 795..800
; OTHER INFORMATION: n=a, g, c or t
US-09-671-317-439

Query Match 3.8%; Score 86.2; DB 4; Length 1001;
Best Local Similarity 64.8%; Pred. No. 8.1e-13;
Matches 138; Conservative 0; Mismatches 74; Indels 1; Gaps 1;
QY 1391 AACCAAGCGGAGATTAAGGGAGGAGTGAAGAGGTGCGAGGCGTTGATAACGACGAAG 1450
Db 999 ATCTCAAG 940
QY 1451 AAAGCGAAGACGAGCGCTAGACGACGAAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1510
Db 939 AAG 880
QY 1511 ATAATGCGGAG 1569
Db 879 AAGAAG 820
QY 1570 GAAG 1602
Db 819 GAAG 787

RESULT 4
US-08-742-185-101
; Sequence 101, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI94-07A2
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43795 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101
Query Match 3.7%; Score 84.6; DB 3; Length 43795;
Best Local Similarity 61.6%; Pred. No. 1.2e-11;
Matches 135; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1386 AAGTAAACCAAGCGGAGAGATTAAGGGAGGAGTGAAGAGGTGCGAGGCGTTGATAACGA 1445
Db 38932 AAAAAAAAAAAAAAAAAAG 38891
QY 1446 CGAAGAAAGCGAAGACGAGCGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1505
Db 38892 AGCGAGATGAG 38951
QY 1506 AGAGGATTAATGCGGAG 1565
Db 38952 GAAGGAAGCGGAG 39011
QY 1566 AGCGGAG 1604
Db 39012 AGAAG 39050

RESULT 5
US-08-574-959A-8
; Sequence 8, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
US-08-574-959A-8
Query Match 3.7%; Score 83.6; DB 2; Length 3211;
Best Local Similarity 63.4%; Pred. No. 6.7e-12;
Matches 128; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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1404		
1405	AGGAGGAAGACGAGAGGAGGAG	2464
1408		
1409		
1410		
1411		
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1454		
1455		
1456		
1457	AAAGCAAGCCGTAGAAGACGAAGGCGCGAAGACGAAACTTCGGAAGAGGATAATG	1516
1460		
1461		
1462		
1463		
1464		
1465	AGGAAGAAGAGGAAGAGGAGGAGAGACTTTTCAGGAAGAGGAGAGAGATGAAGAGGAATATT	2524
1468		
1469		
1470		
1471		
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1514		
1515		
1516		
1517	GGCAGACGAGAGCAACCGCCGAGAGAGAAACCGAAGAGTTGTATGAAGCCGCAAGAGG	1576
1520		
1521		
1522		
1523		
1524		
1525	TTGACGACGAGAGAGGAGGAGAGAGTTTCGGAAGAGAAATTTGAGGAGAGAGAGGTC	2584
1528		
1529		
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1554		
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1556		
1557	AGGAAGTTGAAGAACCCGAGA	1598</

RESULT 6
 US-09-357-014-8
 ; Sequence 8, Application US/09357014
 ; Patent No. 6291645
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaekyoon Shin, Insil Jung, Ratna K. Vadlamudi
 ; AND JACK L. STROMINGER
 ; TITLE OF INVENTION: P62 POLYPEPTIDES. RELATED POLYPEPTIDES
 ; AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/357,014
 ; FILING DATE: 19-Jul-1999
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/574,959
 ; FILING DATE: <unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: DFN-008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3211 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 439..3157
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-357-014-8

[illegible]

1457	AAGACGAAGCCGTGAGACGACGAGCGCGCGAAGACCAAACTTCGGAAGAGGATAATG	1516
QY		
2465	AGGAAGAGGAGGAGAGGAGGAAGACTTTGAGAGAGGAGGAGGATATTT	2524
Db		
1517	GCGAAGACGAAGAAGCAACCGCCGACGAGAAACCGAAGATTGATGAAGCCGAAAGG	1576
QY		
2525	TTGAAGAGGAGAGAGAGGAGGAAGAGAGTTTGAGGAGGAATTTGAGGAGAGAGAGGTTG	2584
Db		
1577	AGGAAGTTGAGAACCCCGAAGA	1598
QY		
2585	AGTTAGAGGAGAGGAAGAAGA	2606
Db		

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RESULT 7
US-08-574-959A-6
; Sequence 6, Application US/08574959A
; Patent No. 5962224
;
GENERAL INFORMATION:
;
APPLICANT: Jaekyoon Shin, Insil Jeoung, Ratna K. Vadlamudi
;
APPLICANT: Jaekyoon Shin, Insil Jeoung, Ratna K. Vadlamudi
;
TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
;
TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
;
NUMBER OF SEQUENCES: 22
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: LAHIVE & COCKFIELD
;
STREET: 60 State Street, Suite 510
;
CITY: Boston
;
STATE: Massachusetts
;
COUNTRY: USA
;
ZIP: 02109-1875
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
;
COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
;
SOFTWARE: Patentin Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/08/574,959A
;
FILING DATE: 19-DEC-95
;
ATTORNEY/AGENT INFORMATION:
;
NAME: Mandragouras, Amy E.
;
REGISTRATION NUMBER: 36,207
;
REFERENCE/DOCKET NUMBER: DFN-008
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: (617)227-7400
;
TELEFAX: (617)227-5941
;
INFORMATION FOR SEQ ID NO: 6:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 3901 base pairs
;
TYPE: nucleic acid
;
STRANDEDNESS: single
;
TOPOLOGY: linear
;
MOLECULE TYPE: cDNA
;
FEATURE:
;
NAME/KEY: CDS
;
LOCATION: 439..3847
;
US-08-574-959A-6

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	Query Match	3.7%	Score 83.6;	DB 2;	Length 3901;
	Best Local Similarity	63.4%;	Pred. No. 7.3e-12;		
	Matches 128;	Conservative	0;	Mismatches 74;	Indels 0; Gaps 0;
QY	1397	AGGCGGAATAAAGGGGAGGATCAACAGAGGTGCAGCGTTGTATAACGACGAGAAGACG	1456		
Db	3095	AGGAGGAAGAGGGAAGAGAGCAAGACAAGAGNAGNAGAGGAGGAGNAGAAGAAAG	3154		
QY	1457	AAGACGAAGCCCTAGAACACGAAGCGCGCGAAGAGACGAAAATTTCGAAGAGCATTAATG	1516		
Db	3155	AGGAACAGAGGAAGAGGAGGAACACTTTTGAGGAAGAGCAGAGGATGAAGAGGAATATT	3214		
QY	1517	GCGAAGACGAAGACAAACC CGCAAGACGAAGAAACCGAAGAGTGTGATGAAGCCGAAGAGG	1576		
Db	3215	TTCAGAGAGCAAGAGGAGAGGAAGAGATTTTGAGGAGAGAAATTTGACGAGNAGNAGAGGTG	3274		

Thu Aug 26 10:18:17 2004

1913 ATGGCAACGGTTTCCAGCGACAGCGGCGCTCGGGAGAGCGGCATCAATCTTTCGGAA 1972
1927 AGGCAACGGCTTTGAAGGTACGCGCAAACTGCTGAGTCAGGTTTGTATCTCGATCAA 1986
1973 ATGGTTCCAGCAGCCCAACATTCAGCTAGTATCTTCGTGTAGAAGGAGGATTTT 2032
1987 AAAATACCAACCGCAGCCTAAGGCATATATCACAGATGCCAAGTAAAGGCGGTTT 2046
2033 ACGGCCCGCAGCGCGGAATTGGCGGTACTATTTCATTAATGATGGGAA 2085
2047 ACGGGCTTAAGCCAGAGATTGGCGGATGTTTGCCTATCCGGCGCATAAA 2099
RESULT 11
US-08-867-921-7
; Sequence 7, Application US/08867921
; Patent No. 6326350
; GENERAL INFORMATION:
; APPLICANT: JACOBS, Eric
; APPLICANT: LEGRIN, Michele
; APPLICANT: MAZARIN, Veronique
; APPLICANT: BOUCHON-THEISEN, Bernadette
; APPLICANT: SCHRYVERS, Anthony B.
; APPLICANT: BLOCH, Marie-Aline
; TITLE OF INVENTION: DNA FRAGMENTS CODING FOR THE TRANSFERRIN
; TITLE OF INVENTION: RECEPTOR OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,921
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/445,472
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/361,469
FILING DATE: 22-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,053
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92 07493
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 016100-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2230 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: DNA which encodes Tbp2 subunit of transferrin
ORGANISM: receptor

ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,194
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,469
FILING DATE: 22-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,053
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92 07493
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 016100-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2230 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: DNA which encodes Tbp2 subunit of transferrin
ORGANISM: receptor
STRAIN: Neisseria meningitidis IM2169
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 60..119
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 120..2192
FEATURE:
NAME/KEY: CDS
LOCATION: 60..2192
US-08-448-194-7
Query Match 3.4%; Score 77.4; DB 3; Length 2230;
Best Local Similarity 52.8%; Pred. No. 2.4e-10;
Matches 218; Conservative 0; Mismatches 186; Indels 9; Gaps 2;
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1690 TGTTCTCCAGGCGGTACCGATGAAAAGAGATTCCAAACCGACCAACGTCGTTT 1749
1739 ATACCGGCATTTGGAGAGCGGTATCGCAACCCATTCATGGACAATCAGCGGATG 1798
1750 ATCGGGGTCCTTGTACGGCATATTCGCAACGCGCAAGCTGGAGCGGCGATCTCTG 1809
1799 AAAAGCGGCA-----AAACAGAAATTACGTTGATTTTCACAAGAAATCGATTCCG 1852
1810 ATAAAGAGGCGGCAACGCGCGGAATTACTGTGAATTTTCCGATATAAAATATACG 1869
1853 GAAAGCTACGAGCAAAACCGCGGTAGAACTGCTTCCATTTGAGACGCGGAGATTG 1912
1870 GCAAGTTAACCGCTGAAAACAGGCGGCGCAACCTTTACCATT---GAGGGAATGATTC 1926

Thu Aug 26 10:18:17 2004

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QY 1457 AAGACGAAGCCGTAGAACGACGAGCGCGGAGAGAGCGAACTTCCGAAGAGGATATG 1516
Db 1121 AGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGAGGAGGAGGAGGAGC 1180
QY 1517 GCGAAGACGAAGACGACCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1576
Db 1181 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1240
QY 1577 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1636
Db 1241 AGGAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1300

RESULT 14
US-09-410-399-1
; Sequence 1, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; APPLICANT: Cotter, Murray A.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; TITLE OF INVENTION: to Genomic Host DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/09/410,399
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

Query Match 3.3%; Score 73.6; DB 4; Length 3489;
Best Local Similarity 56.7%; Pred. No. 2.9e-09;
Matches 136; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1397 AGCGGAGAGATGAAGCGGAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1456
Db 1061 AGGAGGATGACGAGGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACG 1120
QY 1457 AAGACGAAGCCGTAGAACGACGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1516
Db 1121 AGGAGGATGACGAGGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACG 1180
QY 1517 GCGAAGACGAAGAGCAACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1576
Db 1181 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1240
QY 1577 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1636
Db 1241 AGGAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1300
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RESULT 15
US-08-770-379-20/c
; Sequence 20, Application US/08770379.
; Patent No. 5849564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20

Query Match 3.3%; Score 73.6; DB 2; Length 32207;
Best Local Similarity 56.7%; Pred. No. 9e-09;
Matches 136; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1397 AGCGGAGAGATGAAGCGGAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1456
Db 20936 AGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACG 20877
QY 1457 AAGACGAAGCCGTAGAACGACGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1516
Db 20876 AGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACG 20817
QY 1517 GCGAAGACGAAGAGCAACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1576
Db 20816 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20757
QY 1577 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1636
Db 20756 AGGAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20697

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Job time : 166.35 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 23:48:06 ; Search time 1138.6 Seconds
(without alignments)
9777.159 Million cell updates/sec

Title: US-10-735-098-7
Perfect score: 2262
Sequence: 1 atgtgttaaacgaattatgg.....tcgaggagtggaataatga 2262

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2262	100.0	2262	17	US-10-735-098-7
2	1465.2	64.8	2277	17	Sequence 7, Appli
3	1442.6	63.8	2226	13	Sequence 1, Appli
4	1442.2	63.8	2226	13	Sequence 29815, A
5	1291.8	57.1	2124	17	Sequence 5, Appli
6	1250.6	55.3	2169	17	Sequence 9, Appli
7	730	32.3	1000	17	Sequence 3, Appli
8	169.2	7.5	3300	17	Sequence 15, Appli
9	100.2	4.4	31124	13	Sequence 80, Appli
10	98.4	4.4	37265	13	Sequence 463, Appl
11	96	4.2	374849	13	Sequence 49, Appli
12	94.2	4.2	635	13	Sequence 1627, Ap
13	94.2	4.2	635	16	Sequence 269927,
14	91.6	4.0	96596	12	Sequence 269927,
					Sequence 70, Appli

15	91	4.0	522	14	US-10-101-487-71	Sequence 71, Appl
16	91	4.0	530	14	US-10-101-487-73	Sequence 73, Appl
17	91	4.0	554	14	US-10-101-487-69	Sequence 69, Appl
18	91	4.0	554	14	US-10-101-487-106	Sequence 106, Appl
C 19	90	4.0	305	9	US-09-864-761-19262	Sequence 19262, App
C 20	90	4.0	496	9	US-09-864-761-2534	Sequence 2534, Ap
C 21	87.6	3.9	143899	10	US-09-972-546-15	Sequence 15, Appl
C 22	87.4	3.9	68233	16	US-10-034-650-31	Sequence 31, Appl
C 23	86.4	3.8	39443	16	US-10-085-117-313	Sequence 313, App
C 24	86.2	3.8	929	13	US-10-294-934-14	Sequence 14, Appl
C 25	86.2	3.8	1001	13	US-10-294-934-439	Sequence 439, App
C 26	86.2	3.8	96602	16	US-10-085-117-61	Sequence 61, Appl
C 27	85.8	3.8	115223	17	US-10-322-281-773	Sequence 773, Appl
C 28	85	3.8	45980	10	US-09-957-956-6	Sequence 6, Appli
C 29	85	3.8	96597	12	US-10-052-482-103	Sequence 103, App
C 30	84.6	3.7	276	9	US-09-864-761-20595	Sequence 20595, A
C 31	84.6	3.7	1848	13	US-10-027-632-98794	Sequence 98794, A
C 32	84.6	3.7	1848	13	US-10-027-632-98795	Sequence 98795, A
C 33	84.6	3.7	1848	16	US-10-027-632-98794	Sequence 98795, A
C 34	84.6	3.7	1848	16	US-10-027-632-98795	Sequence 98794, A
C 35	84.6	3.7	32069	15	US-10-004-113-7	Sequence 98795, A
C 36	84.6	3.7	96595	12	US-09-997-722-43	Sequence 7, Appli
C 37	84.2	3.7	438	9	US-09-864-761-4988	Sequence 43, Appl
C 38	83.6	3.7	3120	13	US-10-112-944-191	Sequence 4988, Ap
C 39	83.6	3.7	122859	13	US-10-087-192-37	Sequence 191, App
C 40	82.6	3.7	193853	13	US-10-087-192-37	Sequence 37, Appl
C 41	82.4	3.6	225883	15	US-10-087-192-1663	Sequence 1663, Ap
C 42	82	3.6	551	15	US-10-175-523-57	Sequence 57, Appl
C 43	82	3.6	927	16	US-10-029-386-5590	Sequence 57, Appl
C 44	82	3.6	1032	16	US-10-369-493-26106	Sequence 5590, Ap
C 45	82	3.6	3818	13	US-10-369-493-26107	Sequence 26106, A
					US-10-112-944-663	Sequence 26107, A
						Sequence 663, App

ALIGNMENTS

RESULT 1
US-10-735-098-7
; Sequence 7, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10735,098
; PRIOR FILING DATE: 2003-12-12
; PRIOR FILING DATE: 2000-02-15
; PRIOR FILING DATE: 2000-02-15
; PRIOR FILING DATE: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR FILING DATE: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain M990
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(2259)
US-10-735-098-7

Query Match 100.0%; Score 2262; DB 17; Length 2262;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTAACCGAATATGCGCGCATTCGTTGTCCTTACTTTAGCACTTGTATC 60
DB 1 ATGTGTAACCGAATATGCGCGCATTCGTTGTCCTTACTTTAGCACTTGTATC 60

QY	61	GGCGGCAATTTTCGGCGTACAGCTGTTGTGCGAATCAACGCGGACCGCGCCAACTCTGTCA	120	QY	1141	AAAATCTTGATTTCTTAAATAATTTTCGGTTGACGAGCGGACTGATGCGCATGCCGTAAG	1200
Db	61	GGGGCAATTTTCGGCGTACAGCTGTTGTGCGAATCAACGCGGACCGCGCCAACTCTGTCA	120	Db	1141	AAAATCTTGATTTCTTAAATAATTTTCGGTTGACGAGCGGACTGATGCGCATGCCGTAAG	1200
QY	121	GATTCGCAATCTTCCAAATCTTCGGGTAAGCTCTCCAGCTCTCGCGGACCGCTTCGGTA	180	QY	1201	TTTGCCCATTTTCTCTATGCGCGATTTTGGTTCATCCGACAAACTTCTTGTGCGAAGGCGT	1260
Db	121	GATTCGCAATCTTCCAAATCTTCGGGTAAGCTCTCCAGCTCTCGCGGACCGCTTCGGTA	180	Db	1201	TTTGCCCATTTTCTCTATGCGCGATTTTGGTTCATCCGACAAACTTCTTGTGCGAAGGCGT	1260
QY	181	GAATACACGCGGTCAAGCGGCGCGCTCGGTGCGCAATTCGCGTCCGCAAGCGGAAT	240	QY	1261	GAATTCCTTTTGGTAAACGGAACAAATCATCAAGCTTCCGACGCGCAGGAAAATGACC	1320
Db	181	GAATACACGCGGTCAAGCGGCGCGCTCGGTGCGCAATTCGCGTCCGCAAGCGGAAT	240	Db	1261	GAATTCCTTTTGGTAAACGGAACAAATCATCAAGCTTCCGACGCGCAGGAAAATGACC	1320
QY	241	ATCGCAATCTTTGTATAAATATGTAATTCCTCAATAGTACAGGCGAGAGAT	300	QY	1321	GTCCGTCTGTTGCGGACTTTTGTGACCTATGTGAAACTCGACCGGATAAACCCTATGAC	1380
Db	241	ATCGCAATCTTTGTATAAATATGTAATTCCTCAATAGTACAGGCGAGAGAT	300	Db	1321	GTCCGTCTGTTGCGGACTTTTGTGACCTATGTGAAACTCGACCGGATAAACCCTATGAC	1380
QY	301	CTGCGCTCAAGAGAGGATATCTGTTTGTAGACGGTACCGCAAGAAACAGGCTGAC	360	QY	1381	CCGCAAGTAAACCAAGAGGCGGAGATAAAGGCGAGGATGAAGGGTTCGAGGGCTTGAT	1440
Db	301	CTGCGCTCAAGAGAGGATATCTGTTTGTAGACGGTACCGCAAGAAACAGGCTGAC	360	Db	1381	CCGCAAGTAAACCAAGAGGCGGAGATAAAGGCGAGGATGAAGGGTTCGAGGGCTTGAT	1440
QY	361	AAATCTTAAAGAGAAATCAACGCGGCGATCTTAATGACCAATCTACAGTCCGATTA	420	QY	1441	AACGACGAAGAAAGCGAAGACGAGCCGTAGAAGACGAAGCGCGGGAAGACGAAACT	1500
Db	361	AAATCTTAAAGAGAAATCAACGCGGCGATCTTAATGACCAATCTACAGTCCGATTA	420	Db	1441	AACGACGAAGAAAGCGAAGACGAGCCGTAGAAGACGAAGCGCGGGAAGACGAAACT	1500
QY	421	AAAGATGATGCTATCAATATAAATATGTCGGGCGCGATATGTTTATAGATATGGA	480	QY	1501	TCCGAAGAGGATATTCGGCGAAGACGAAAGCAACCCGCGAAGAAACCGGAAGATT	1560
Db	421	AAAGATGATGCTATCAATATAAATATGTCGGGCGCGATATGTTTATAGATATGGA	480	Db	1501	TCCGAAGAGGATATTCGGCGAAGACGAAAGCAACCCGCGAAGAAACCGGAAGATT	1560
QY	481	ACAGATGAATCGACAGAACTCAGCGGTAGCGGTTTACCCACCGCTTAGGTTATGAC	540	QY	1561	GATGAAGCCGAGAGGAGGAGGAGTTGAAGAACCCGAAAGAAAATCCCGCGAGAAAGCAAC	1620
Db	481	ACAGATGAATCGACAGAACTCAGCGGTAGCGGTTTACCCACCGCTTAGGTTATGAC	540	Db	1561	GATGAAGCCGAGAGGAGGAGGAGTTGAAGAACCCGAAAGAAAATCCCGCGAGAAAGCAAC	1620
QY	541	GCTTTTGTATATTTTCGGGAGACGTCCTTCCCAATCTTTACCGAGTCCGGGACGGTG	600	QY	1621	GGCGTTTACGGCAGCATCTGCTTCCCTAGAGGCTCTAAGGCGAGGAGACATCGACCTT	1680
Db	541	GCTTTTGTATATTTTCGGGAGACGTCCTTCCCAATCTTTACCGAGTCCGGGACGGTG	600	Db	1621	GGCGTTTACGGCAGCATCTGCTTCCCTAGAGGCTCTAAGGCGAGGAGACATCGACCTT	1680
QY	601	GAATATCTGGTAACTGGCAATATATGACCGATGCCAAACGTCATCGACAGTCAAGCG	660	QY	1681	TTCTCTGAAAGGATTCGCGACGCGGAGGAGTATTCGCAAGGCGGAGGAGGAGGAGTAT	1740
Db	601	GAATATCTGGTAACTGGCAATATATGACCGATGCCAAACGTCATCGACAGTCAAGCG	660	Db	1681	TTCTCTGAAAGGATTCGCGACGCGGAGGAGTATTCGCAAGGCGGAGGAGGAGGAGTAT	1740
QY	661	GTGGCATGCAATTTGGGTTATATCAATTTATGTAAAGTATGAGTTCGTTGCACTTCT	720	QY	1741	ACCGGACCTTGGGAGCGGTATCGCAAAACCCATTCATGCGGACAAATCAGGCGGATGAA	1800
Db	661	GTGGCATGCAATTTGGGTTATATCAATTTATGTAAAGTATGAGTTCGTTGCACTTCT	720	Db	1741	ACCGGACCTTGGGAGCGGTATCGCAAAACCCATTCATGCGGACAAATCAGGCGGATGAA	1800
QY	721	TATGCGGCTAAGGATGTCGACGAAAGGGAAGGAGCATCTGCCAAATATACGGTTGATTT	780	QY	1801	AAAGCGGCAAAAGCAGAAATTTACCGTTGATTTTCGACAGAAATCGATTTCCGAAAGCTG	1860
Db	721	TATGCGGCTAAGGATGTCGACGAAAGGGAAGGAGCATCTGCCAAATATATACGGTTGATTT	780	Db	1801	AAAGCGGCAAAAGCAGAAATTTACCGTTGATTTTCGACAGAAATCGATTTCCGAAAGCTG	1860
QY	781	GATAACAAACCAATGATGCAAGCTGATTAATAATCAGTATGTCGGAATAAAGAT	840	QY	1861	ACGAGCAAAAACGCGGTAGAACTCTGTTCCATATTTGAAGACGCGCAAGATTGATGCAAC	1920
Db	781	GATAACAAACCAATGATGCAAGCTGATTAATAATCAGTATGTCGGAATAAAGAT	840	Db	1861	ACGAGCAAAAACGCGGTAGAACTCTGTTCCATATTTGAAGACGCGCAAGATTGATGCAAC	1920
QY	841	GAACCCAAAACCGCTGACCATTTACGACATTTACGAAAATTTGACGCGCAACCGCTTT	900	QY	1921	GGTTTCCACGCGACGCGGCTCTCGGAGAGCGGCTCAATCTTTTCGGAATGTTGTCG	1980
Db	841	GAACCCAAAACCGCTGACCATTTACGACATTTACGAAAATTTGACGCGCAACCGCTTT	900	Db	1921	GGTTTCCACGCGACGCGGCTCTCGGAGAGCGGCTCAATCTTTTCGGAATGTTGTCG	1980
QY	901	ACCGGAGTCCCAAGGTCATCTGATTTAGCGAAAACCTTCCCGGTATAGCGGTTG	960	QY	1981	ACCGACCCCAAAACATTTCCAAAGCTAGTAACTCTTCGTTGAGAGGAGGATTTTACGCGCG	2040
Db	901	ACCGGAGTCCCAAGGTCATCTGATTTAGCGAAAACCTTCCCGGTATAGCGGTTG	960	Db	1981	ACCGACCCCAAAACATTTCCAAAGCTAGTAACTCTTCGTTGAGAGGAGGATTTTACGCGCG	2040
QY	961	TTTTTTCATGCGGATCGGCTGAGGCGGTTTTCGCGGATTAACGGAGAA	1020	QY	2041	CAGCGCGGGAATTTGGCGGTACTATTTTCAATAATGATGCGGAATCTCTTAGTATAACT	2100
Db	961	TTTTTTCATGCGGATCGGCTGAGGCGGTTTTCGCGGATTAACGGAGAA	1020	Db	2041	CAGCGCGGGAATTTGGCGGTACTATTTTCAATAATGATGCGGAATCTCTTAGTATAACT	2100
QY	1021	GAGCTTCGCGACCGGTTTATCAGCAACGACAGCGTATTTCCGCGTATTTCCGAGGCAAA	1080	QY	2101	GAATAATTTCAAAATGAAGCTGAAGTGAAGTTGAAGTTGAAGCTGAAGTTGAAGTTGAA	2160
Db	1021	GAGCTTCGCGACCGGTTTATCAGCAACGACAGCGTATTTCCGCGTATTTCCGAGGCAAA	1080	Db	2101	GAATAATTTCAAAATGAAGCTGAAGTGAAGTTGAAGTTGAAGCTGAAGTTGAAGTTGAA	2160
QY	1081	AAAAACAGAGACGAAACGCGAGGAGATCAAAAACCTTCCCGCTTCGGAACACACC	1140	QY	2161	GTTGAAGCTGATTTGGCAACAGTTAGAACCTGATGAAGTTAAACACAACTTCGCGGTG	2220
Db	1081	AAAAACAGAGACGAAACGCGAGGAGATCAAAAACCTTCCCGCTTCGGAACACACC	1140	Db	2161	GTTGAAGCTGATTTGGCAACAGTTAGAACCTGATGAAGTTAAACACAACTTCGCGGTG	2220
				QY	2221	GTATTCGGTCCGAGAGAGATATGACGAGGTGGAAAAATGA	2262

Db 2221 GTATTCGGTCCGAAGAAAGATATGACGAGGTGGAAAAATGA 2262

RESULT 2

US-10-735-098-1
; Sequence 1, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; PRIORITY FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2277
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain BNCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(2274)
US-10-735-098-1

Query Match 64.8%; Score 1465.2; DB 17; Length 2277;
Best Local Similarity 81.1%; Pred. No. 0;
Matches 1835; Conserved 0; Mismatches 343; Indels 84; Gaps 8;
QY 1 ATGTGTAACCGAATATATGCGGCAATCTCTTGTGTCCTTACCTTTAGCATCTGTATC 60
Db 100 ATGTGTAACCGAATATATGCGGCAATCTCTTGTGTCCTTACCTTTAGCATCTGTATC 159
QY 61 GCGCGCAATTTTCGGGTACAGCTCTTGTGTAATCAAGCGCGACCGGCCCACTCTGTCA 120
Db 160 GCGCGCAATTTTCGGGTACAGCTCTTGTGTAATCAAGCGCGACCGGCCCACTCTGTCA 207
QY 121 GATTCGAATCTTCCCAATCTGCGGTAAGCTCTGCTCCAGCTCTGCGGACCTTCGGTA 180
Db 208 TACCCCGTCACTTCAAGTCTAAGGACGTTCCCACTCGCCCGCTGCCAACTTCTATA 267
QY 181 GAAATACGCGCGGTCAAGCGCGCGCGCTGCTGCGGCAATGCGCTGCGGCAATGCGGTA 240
Db 268 GAAATACGCGCGGTCAAGCGCGCGCGCTGCTGCGGCAATGCGCTGCGGCAATGCGGTA 327
QY 241 ATCGCAACTTTTGATAAAATGTAATGAAATCCCAATAGTAAGCAGGACGAGGAGTAT 300
Db 328 ACTGCTTTTCATCGTGAAGATGCAAGCAATTCGAATAGCAACAGCAGAGAGAAAG 387
QY 301 CTGCGCTCAAGAGAGAGATATCTCTTTTGAAGCGGTACGCGGCAAGAGAGAGGCTGAC 360
Db 388 CTGCGCTTCAAGAGAGATATCTCTTTTGAAGCGGTACGCGGCAAGAGAGAGGCTGAC 447
QY 361 AAATCTTAAAGAGAAATCAAGCGCGGCAATCTTAAAGCAACCACTTACAGCTCGATTA 420
Db 448 CAATCTTAAAGAGAAATCAAGCGCGGCAATCTTAAAGCAACCACTTACAGCTCGATTA 507
QY 421 AAAGATGATGCGTATCAATATAAATATGTCGCGCGCGGATATGTTATATCTAGATATGA 480
Db 508 GAAATATAAATAATATGTTATATAAATTTGTAGTGCAGGTATGTTATA---TGTAAGGGA 564
QY 481 ACAGATGAATCGAACAGAACTCAGCGGTTAGCGGTTACCGGTTAGCTTATGATGAC 540
Db 565 AAAGATGAATTAAGTGGACTTCAGATTACAAGCAGTTTTCACACCGCTTAGCTTATGAC 624

QY 541 GGTGTTGTATATATTCGCGAGAACGTCCTTCCCAATCTTTTACGAGTGGGAGAACGGTG 600
Db 625 GGTGTTGTATATATTCGCGAGAACGTCCTTCCCAATCTTTTACGAGTGGGAGAACGGTG 684
QY 601 GAATATTTCTGTTAACTGGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTGACGGC 660
Db 685 GAATATTTCTGTTAACTGGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTGACGGC 744
QY 661 GTTGGCATTTGACAAATTTGGTTATATACATTTTATGTTAAACGATGTTGTTGCAACTTCT 720
Db 745 GTTGGCATTTGACAAATTTGGTTATATACATTTTATGTTAAACGATGTTGTTGCAACTTCT 804
QY 721 TATCGCGCTTAAGGATGTCGACGAAAGGAAAGCATCTGCCCAATATATACGTTGATTTT 780
Db 805 TATCGCGCTTAAGGATGTCGACGAAAGGAAAGCATCTGCCCAATATATACGTTGATTTT 864
QY 781 GATAACAAAACCATGAATGGCAAGCTGATTTAAATATCAGTATGTCGAAATATAAAGAT 840
Db 865 GGTAAACAAAACCATGAATGGCAAGCTGATTTAAATATCAGTATGTCGAAATATAAAGAT 918
QY 841 GAAACCCAAAACCATGACCATTTTACGATTTTACGATTTTACGATTTTACGATTTTACG 900
Db 919 GAAAGCAAAAACCATGACCATTTTACGATTTTACGATTTTACGATTTTACGATTTTACG 978
QY 901 ACCGCGAGTGGCAAGGTCAATCTCTGATTTTACGAAACCTTGCCTGATTAATGAGGTTTG 960
Db 979 ACCGCGAGTGGCAAGGTCAATCTCTGATTTTACGAAACCTTGCCTGATTAATGAGGTTTG 1038
QY 961 TTTTTCATGCGGATGCGGATCAGCGGCTTACGAGGCGGTTTTCGCGGATTAACGAGAA 1020
Db 1039 TTTTTCATGCGGATGCGGATCAGCGGCTTACGAGGCGGTTTTCGCGGATTAACGAGGAA 1098
QY 1021 GAGCTTTCGCGGACGCTTTTATCAGCAACGACGATTTGCGGTATTCGCGGTATTCGAGGCA 1080
Db 1099 GAGCTTTCGCGGACGCTTTTATCAGCAACGACGATTTGCGGTATTCGCGGTATTCGAGGCA 1158
QY 1081 AAAACAGAGACAGCAACGACGATACAAACCTGCGCTGCGGCTTGGAAACACACACC 1140
Db 1159 CA-----AAATAGCCCCGCTGCGGCTTGGAAACACACACC 1191
QY 1141 AAAATCTTGAATCTTAAATAATTCGCTTACGAGGCGATGATGCGCATGCGCGTAAG 1200
Db 1192 AAAATCTTGAATCTTAAATAATTCGCTTACGAGGCGATGATGCGCATGCGCGTAAG 1251
QY 1201 TTTGCCATTTCTCTATGCGGATTTTGGTATCCCGACAACTTTCTTGTGCAAGGCGT 1260
Db 1252 TTTGCCATTTCTCTATGCGGATTTTGGTATCCCGACAACTTTCTTGTGCAAGGCGAT 1311
QY 1261 GAAATCTTGTGTAACGAGAAACAAATCATCAAGCTTCCGCGGCGGCAAGAAATGACC 1320
Db 1312 GAAATCTTGTGTTAGCAGAGAGAAACCATGAGCTTCCGCGGCGGCAAGAAATGACC 1371
QY 1321 GTCGGTCTTGTGCGATTTTGAATCTTGTGAACTCGGACGATTAATAACCGATCGC 1380
Db 1372 GTGAGTCTTGTGCGATTTTGAATCTTGTGAACTCGGACGATTAATAACCGATCGC 1431
QY 1381 CCGGCAAGTAAACCAAGCGGAGAGATAAGGGGAGGATGAAGGGTGCAGCGGTTGAT 1440
Db 1432 CCGCGCGCAACCGAGGCG-----GAGGAGAGAGGATTCGACATTTGAT 1479
QY 1441 AACGAG 1500
Db 1480 AATGGCGAG 1539
QY 1501 TCGAAG 1560
Db 1540 GCAGGAG 1581
QY 1561 GATGAGCGAG 1620
Db 1582 GAAG 1641

RESULT 3
US-10-282-122A-29815
; Sequence 29815, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335

Qy	301	CTGCCGTCAAAGAGAGATATCCTCTGTTTATACACGGTACGCCGGAAGAACAGCCTCAC	360
Db	289	CTGCTGTTTAAAGAGGTGATGTTCTGTGTTTTATACGGTTCCAAAAGATATAACTTCAG	348
Qy	361	AAACTTTAAAAGAGAAATCAACGGACGGCATCCTTAATGCACCAATCTACACGTCGAAATTA	420
Db	349	CAGCTTTAGGATAAAATTCATCAACGCAATCCTAATGTAGAAATTAGGACATCAGAAAT	408
Qy	421	AAAGATGATCGGTATCAATATAAATATGTCGGGCCGGATATGTTTATACATAGATATCGA	480
Db	409	GAAATAAAAAATATGTTTATCAATTTGTAGATGCAGGTTATGTATATATACACAAGGGA	468
Qy	481	ACAGTGAATCGAACAACTCAGGCGGTAAAGCGGTTACCCACCGCTTAGGTTTATGAC	540
Db	469	AAAGATGAAATTTGATGGACATTCAAATCAAGACAGTTTACTACCGGTTTGTTTATGAC	528
Qy	541	GGTTTTGTATATATTCCGGAGAACGTCCTTCCCAATCTTTACCGAGTGGCGGAACGGTG	600
Db	529	GGTTTTGTATATTTCGGAGAACATCCTTCGCAATCTTTACCGAGCGCGGAACGGTG	588
Qy	601	GAATATTCGTGTAACCTGCAATATATGACCGATGCCAACGTCATCGACAGCTCAGGC-	659
Db	589	AAATATTCGGCAACTGGCAATATATGACCGATGCCAATACGTCATCGAACAGGAAGCA	648
Qy	660	--GGTTGGCAATGCAAAATTTGGGTTATATCACATTTTATGTTAAAGATGTTGGTGAAC	717
Db	649	GGAGATCCTAGCGAAGATTTGGGTTATATCGTTTATTACGGTCAAAATGTCGAGAGCA	708

Db	1	ATGTGTAACCGAAATATATGCGGCAATGTCTTGTGTCCTTACTTTTGGCATCTTGTAT	60
Qy	61	GGCGCAATTTCCGCGTACAGCTGTGTGTCGAATCAACGCGCGACCGCGCCAACTCTGTCA	120
Db	61	GGCGCAATTTCCGCGTACAGCTGTGTGTCGAATCAACGCGCGACCGCGCCAACTCTGTCA	108
Qy	121	GATTTCCAAATCTTCCAACTCTGCGGATTAAGCTGCTCAGCTCTGCGGAGCCTTCGGTA	180
Db	109	TACCCCGTCACTTTCAAGTCTAAGGAGCTTCCCACTCGGCCCTGCGCAACCTTCTATA	169
Qy	181	GAATACAGCGCGT-----CAAGCGCGCGCGCTCGGTGCGGCAATGCGGCTCCCAAGG	234
Db	169	GAATACAGCGCGT-----CAAGCGCGCGCGCTCGGTGCGGCAATGCGGCTCCCAAGG	228
Qy	235	CGGAATATCGCACTTTTGATAAAATGGAATGGAATTTCCCAATAGTAAGCAGCAGAG	294
Db	229	CGGAATATCGCACTTTTGATAAAATGGAATGGAATTTCCCAATAGTAAGCAGCAGAG	288
Qy	295	GAGTATCTGCGCTCAAGAGAGAGATATCTGTTTGTAGACGCTAGCCGGAAGACAG	354
Db	289	GAATAGCTGTCTTTTAAAGAGGTGATGTTCTGTTTATACGGTTCAAAAAGATATAA	348
Qy	355	GCTGACAACTTAAAGAGAAATCAACGAGCGCATCTTAATGACCAATCTACACGTCC	414
Db	349	CTTCAGTGGCTTAAGGATAAAATTCATCAACGCAATCTTAATGAGAAATTAGGACATCA	408
Qy	415	GATTTAAAGATGATGCGTATCAATATAAATATGTCGCGCGCGGATATGTTTATATACTAGA	474
Db	409	GAATATGAATAAATAATATGTTTATGAAATTTGTTGATGCGCGTTATGATATACTATAA	468
Qy	475	TATGGAACAGATGAATCGAACAGAACTCAGCGCGTGAAGCGGTTACCCACGCTTAGT	534
Db	469	AACGGAACAGATGAATTTGAGTGGACTTCAAAATCGCAAGCACTTTCTTAATCGTTTGGC	528
Qy	535	TATGACGTTTGTATATTTTCCGAGAACGTCCTTCCCAATCTTTACCGAGTGGGGA	594
Db	529	TACGACGTTTGTATATTTTCCGAGAACGTCCTTCCCAATCTTTACCGAGTGGGGA	588
Qy	595	ACGGTGGATATTTCTGTAACCTGGCAATATATGACCGATGCCAAACGTCATCGAGAGT	654
Db	589	ACGGTGCATATTTCCGTTAATTTGCGCAATATATGACCGATGCCAAACGTCATCGAGAGT	648
Qy	655	CAAGC---GGTGGCAATGACAAATTTGGTATATACATTTTATGTAACAGATTTGT	711
Db	649	AAAGCAGGAGATCCTAGCAAGATTTGGTATATCTGTTTATTTACCGTCAAAATGCGGA	708
Qy	712	GCNACTTCTATCGGCTAAGGATGTCGACGAAAGGAAAGCATCTGCAAAATATACG	771
Db	709	GCNACTTCTATCGGCTAAGGATGTCGACGAAAGGAAAGCATCTGCAAAATATACG	768
Qy	772	GTTGATTTTGATAACCAAAACCATGAATGGCAAGCTGATTAATAATCATGATGTCGGAAT	831
Db	769	GTTGATTTTGATAACCAAAACCATGAATGGCAAGCTGATTAATAATCATGATGTCGGAAT	828
Qy	832	AAAAAGATGAACCAAAACCATGACCATTTACGACATTTACTGCAAAATTTGACGCG	891
Db	829	AAAAAGATGAACCAAAACCATGACCATTTACGACATTTACTGCAAAATTTGACGCG	885
Qy	892	AACCGTTTACCGGCTGCAAGCTCAATCTGATTTAGCGAAAAACCTTGGCGGTAAT	951
Db	886	AACCGTTTACCGGCTGCAAGCTCAATCTGATTTAGCGAAAAACCTTGGCGGTAAT	945
Qy	952	GAGCGTTTGTATTTTCCATGCGGATGCGGATCAGCGGCTTGAGGCGGTTTTTTCGGGAT	1011
Db	946	GAGCATTTGTTTTTCCATACGATGCGGATCAGCGGCTTGAGGCGGTTTTTTCGGGAT	1005
Qy	1012	AACGGAAGAGCTTGGCGGAGCTTTATCAGCAACGACACAGCTATTCGCGGTATTC	1071
Db	1006	AAGGGGGAAGCTTGGCGGAGCTTTATCAGCAACGACACAGCTATTCGCGGTATTC	1065
Qy	1072	GCAGCAAAAAACAGACAGCAAGCAACGACAGATACAAACCTTCCGCTCGCTGGA	1131
Db	1066	GCAGCAAAAAACAGACAGCAAGCAACGACAGATACAAACCTTCCGCTCGCTGGA	1125
Qy	1132	AAACACACAAAAATCTTGAATCTCTAAAAATTTCCGTTCCAGGAGCGACTGATGGCCAT	1191
Db	1126	AAACACACAAAAATCTTGAATCTCTAAAAATTTCCGTTCCAGGAGCGACTGATGGCCAT	1185
Qy	1192	GCCCGTAAGTTTGCATTTCCCTATGACCCCGATTTTGGTTCATCCCGCAAACTTCTTGTG	1251
Db	1186	GCCCGCGCTTGCATTTCCCTATGACCCCGATTTTGGTTCATCCCGCAAACTTCTTGTG	1245
Qy	1252	GAAGGGGTGAATTTCTTTTGTAAACGAAAGCAAAATCATCAAGCTTTCGCGAGCGCAGG	1311
Db	1246	GAAGGGGTGAATTTCTTTTGTAAACGAAAGCAAAATCATCAAGCTTTCGCGAGCGCAGG	1305
Qy	1312	AAATATGACCGTCCGCTGCTTTTGTGCACTTTTGTACCTATGTGAAATCTCGACGGAATAA	1371
Db	1306	AAATATGACCGTCCGCTGCTTTTGTGCACTTTTGTACCTATGTGAAATCTCGACGGAATAA	1365
Qy	1372	ACCGATCGCGCGGCAAGTAACCAAGCGGCAAGTAAGGGGAGGATGAAGAGGTTGCA	1431
Db	1366	ACTGACCGCGGCAAGTAACCAAGCGGCAAGTAAGGGGAGGATGAAGAGGTTGCA	1425
Qy	1432	GGCGTTGATTAACGACGAAAGAGC---GAAGACGAAAGCGGTAGAGACGAAGGGCGGAA	1488
Db	1426	GGCGTTGATTAACGACGAAAGAGC---GAAGACGAAAGCGGTAGAGACGAAGGGCGGAA	1485
Qy	1489	GAAGACGAAACTTTCGGAAGAGGATTAATCGCGAAGACGAAGAACCGCCGGAAGAA	1548
Db	1486	GAAGACGAAACTTTCGGAAGAGGATTAATCGCGAAGACGAAGAACCGCCGGAAGAA	1536
Qy	1549	ACCGAAGAGTTGATGAAGCGGAGAGGAGGATTTGAAGAACCGCAAGAAATTCGCGG	1608
Db	1537	AACGAAGCGCGGAGAGGAGGATTTGAAGAACCGCAAGAAATTCGCGG	1596
Qy	1609	GCAGAGGCAAC---GGCGTTTCAGGCGACATCTTCCCTGCGCTAGAGACCTCTAAAGC	1665
Db	1597	GCAGAGGCGCGGTTGTTTCAACGCGATCTTCCGCGCTCGGAGCTCTTAAAGC	1656
Qy	1666	AGGACATCGACCTTTTCTGAAAGGATTCGCGAAGGATTCGCGAAGAACCGGATTTCCGCA	1725
Db	1657	AGGATATCGACCTTTTCTGAAAGGATTCGCGAAGGATTCGCGAAGAACCGGATTTCCGCA	1716
Qy	1726	GAAGCGCGCATTTACCGGCACTTTGGGAAGCGGATTCGCGCAAAACCCATTTCAATGGGAC	1785
Db	1717	GGAAAAGCAGCTATATACCGGCACTTTGGGAAGCGGATTCGCGCAAAACCCATTTCAATGGGAC	1776
Qy	1786	AATCAGCGCGATGAAGAACCGGCAAGCAGAAATTTACCGTTGATTTCCGCAAGAAATCG	1845
Db	1777	AATCAGCGCGATGAAGAACCGGCAAGCAGAAATTTACCGTTGATTTCCGCAAGAAATCG	1836
Qy	1846	ATTTCGGAAGAGCTGACGAGCAAAACCGCGGTGAACCTGCTTTCCATATTTGAAGCGGC	1905
Db	1837	ATTTCGGAAGAGCTGACGAGCAAAACCGCGGTGAACCTGCTTTCCATATTTGAAGCGGC	1896
Qy	1906	AAGATTGATGGCAACGTTTCCAGCGACGCGCACTCGGAGAGCGGCATCAATCTT	1965
Db	1897	GTGATTGAGGCAATGGTTTCCAGCGACGCGGCACTCGGATTAACGCGCATCAATCTT	1956
Qy	1966	TCGGAATATGGTTTCGACCGCAACCCCAAAATTCGAGCTAGTAACTCTTCTGTGAGAGGA	2025
Db	1957	TCGGAATATGGTTTCGACCGCAACCCCAAAATTCGAGCTAGTAACTCTTCTGTGAGAGGA	2016
Qy	2026	GGATTTTTACGCGCGGAGGATTTGGCGGCTACTATTTTCAATATGATGGGAAA	2085
Db	2017	GGCTTTTACGCGCGGAGGATTTGGCGGCTACTATTTTCAATATGATGGGAAA	2076
Qy	2086	TCCTTTAGTATACTGAATAATTTGAAATGAACTGAACTGAACTGAACTGAACT	2145
Db	2077	TCCTTTAGTATACTGAATAATTTGAAATGAACTGAACTGAACTGAACT	2112
Qy	2146	GAAGCTGAAGTTGAAGTTGAAGCTGATGTTGGCAACAGTTAGAACCTGATGAAGTTAAA	2205
Db	2113	GAAGCTGAAGTTGAAGTTGAAGCTGATGTTGGCAACAGTTAGAACCTGATGAAGTTAAA	2169

Db 1066 CAAAAACAGACAGCAAAACGATCAGATACAAATCTGCGCTCTGGAACAC 1125
Qy 1138 ACCAAATCTTGGATCTCTAAATTTCCGTTGACGAGCGACTGATGCCATGCCCGT 1197
Db 1126 ACCAAATCTTGGATCTCTAAATTTCCGTTGACGAGCGACTGATGCCATGCCCGT 1185
Qy 1198 AAGTTTCCATTTCTCTATGCGCGATTTTGGTTCATCCGACAACTTCTTGTGGAAGG 1257
Db 1186 AAGTTTCCATTTCTCTATGCGCGATTTTGGTTCATCCGACAACTTCTTGTGGAAGG 1245
Qy 1258 CGTGAATCTTCTTGTGTAAGAGAAACAAATCAAGTTGCGGACGCGAGAAATG 1317
Db 1246 CGTGAATCTTCTTGTGTAAGAGAAACCAATCGAGTTGCGGACGCGAGAAATG 1305
Qy 1318 ACCGTCGCTGCTTCTGCGACTTTTTCACCTATGTGAATTCGACGGATTAATAACCGAT 1377
Db 1306 ACCATCGTCTTCTGCGATTTTCTGACCTATGTGAATTCGACGGATTAATAACCGAT 1365
Qy 1378 CGCCCGCAAGTAAACCAAGCGGAAGATTAAGGGGAGGATGAAGAGGCTGCGAGCGTT 1437
Db 1366 CGCCCGCGCTCAACCGAAGCGCGAGGATGAAGAGGATTCGACATTTGATATGCGAA 1425
Qy 1438 GATAACGACGAAGAA--CGGAGACGAAGCGGTGAAGACGAAGCGCGGAGAGAC 1494
Db 1426 GAAGCGAAGACGAATTTCCGAGAGATGAACGCGAAGATGAAGTCAACCGAAGAG 1485
Qy 1495 GAAACT-----TCCGAGAGGATATGCGAGACGAAGCAACCGCGGAGAA 1548
Db 1486 GAAGCTGAAGAACCGAAGAGAACTGATGAAGACGAAGAGGAAGAACCCGAGAACT 1545
Qy 1549 ACCGAAGATTTGATGAACCGAAGAGGAGGAGTTGAAGAACCCGAGAAATCGCG 1608
Db 1546 GAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAAATCGCG 1605
Qy 1609 ---CGAAGGCAACGCGGTTTCAGCAGCATCTGCGTCCCTAGAAGCTCTAAAGC 1665
Db 1606 ACAGAGAGGCAACGCGGTTTCAGCAGCATCTGCGCCTCCGAGCTCTAAAGC 1665
Qy 1666 AGGACATCGACTTTTCTGAAAGTATCCGACGCGGAGGAGCAATTCGCGAAAT 1725
Db 1666 AGGACATCGACTTTTCTGAAAGTATCCGACGCGGAGGAGCAATTCGCGAAAT 1725
Qy 1726 GGAACGCGCATTTATACCGCATTTGGAAGCGGATCGGCAACCCATTCATGGGAC 1785
Db 1726 GGAAGACACGCTATACCGCATTTGGAAGCGGATCGGCAACCCATTCATGGGAC 1785
Qy 1786 AATCAGGCGGATG-----AAAAAGCGCAAA 1812
Db 1786 GAAAGCTAGATGCACTACGTCATCAAGAGTAGCTATGCGAATCAAGCGCAAA 1845
Qy 1813 GCAGATTTACGTTGATTTTCAGAAATTCGATTTCCGAAAGCTGACGAGCAAAAC 1872
Db 1846 GCAGATTTGACGTTGATTTTGTGCGAGTTCGCTTTTCAGTAAGTTGACAGAAATAAT 1905
Qy 1873 GGCCTAGAACCTGCTTTCATATTAAGAGCGGATTTGATGCAACGCTTTCCACGCG 1932
Db 1906 GATACACACCGCTTTTATATTAAGAAAGGTGTGATGATGCAACGCTTTCCACGCT 1965
Qy 1933 ACAGCGGCACTCGGAGAGCGCATCAATCTTTCGGGAAATGTTTCGACGACCCAAA 1992
Db 1966 TTGGCGGTACTCTGGAATGTTGTTGATTTGTCGGCAAGGTTGCACTAATCCCAA 2025
Qy 1993 ACATTCAGCTAGTAACTTCTGTTAGAGGAGGATTTTACGCGCGGAGCGCGGAA 2052
Db 2026 AGTTTAAAGCCAGTATCTTCTGTTAGAGGAGGATTTTATGTCGCGGCGGAGAG 2085
Qy 2053 TTGGCGGTACTATTTTCAATAATGATGGAAA 2085
Db 2086 TTGGGTGTTAATATTCGACAGTACCGGAAA 2118

RESULT 7

US-10-343-561-15

; Sequence 15, Application US/10343561
; Publication No. US20040126389A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Dalemans, Wilfried
; APPLICANT: Denoel, Philippe
; APPLICANT: Dequesne, Guy
; APPLICANT: Feron, Christiane
; APPLICANT: Garcon, Nathalie
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Thiry, Georges
; APPLICANT: Thomard, Joelle
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: Vaccines Comprising Outer Membrane
; TITLE OF INVENTION: Vesicles from Gram Negative Bacteria
; FILE REFERENCE: B45260
; CURRENT APPLICATION NUMBER: US/10/343,561
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/EP01/08857
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: EP 00956369.3
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: GB 0103170.7
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-561-15

Query Match 32.3%; Score 730; DB 17; Length 1000;
Best Local Similarity 84.8%; Pred. No. 5.3e-169;
Matches 882; Conservative 0; Mismatches 115; Indels 43; Gaps 4;

Qy 1222 GATTTGTCTATCCCGACAACTTCTGTCGAAGGCGTGAATTCCTTTGGTAAACGAA 1281
Db 1 GATTTGTCTATCCGACAACTTCTGTCGAAGGCGTGAATTCCTTTGGTAAACGAA 60
Qy 1282 GAACAATCATCAAGTTGCCGACGCGAGGAAATGACCGTCGCTGCTTTGTCGACTTT 1341
Db 61 GAGAAACCATCAAGTTGCCGATGCGAGGGAATGACCGTCGCTGCTTTGTCGACTTT 120
Qy 1342 TTGACCTATGTAACCTCGGACGATATAAACCGATCGCCGCAAGTAAACCAAGGCG 1401
Db 121 TTGACCTATGTAACCTCGGACGATATAAACCGCAACCGCGCAAGTAAACCAAGGCG 180
Qy 1402 GAAGATAAGGGGAGGATGAAGAGGTCGAGGCTGATACGACGAGAGAGGAGAC 1461
Db 181 GAAGATAAGGGGAGGATGAAGAGGTCGAGGCTGATACGACGAGAGAGGAGGCG 240
Qy 1462 GAAGCCTAGAACGACGAGGCGGCAAGAGAGCAAACTTCCGAAGAGGATATGCGCA 1521
Db 241 GAAGTTTCCGAAGTGAAGGCGAAGAGCGCAAGAAATCGTCGAAGAGA----- 290
Qy 1522 GACGAAGAACCAACCGCGGAGAGAGAACCCGAGAGGATGATGAAGCGGAGGAGAA 1581
Db 291 -----ACCGGAAGAGAGAGCTGAAGAGGAGAGAGTGAACCAAGAA 333
Qy 1582 GTTGAAGAACCCGAGAAATTCGCGGCAAGAG--GGAACGCGGTTTACGAGCATC 1638
Db 334 GTTGAAGAACCCGAGAAATTCGCGGACAGAAAGAGGCGGAGCGGTTTCAACGCGCATC 393
Qy 1639 CTGCTGCGCTAGAACCTCTAAAGGAGGGAATCGACCTTTTCTGAAAGGATTCGCG 1698
Db 394 CTGCTGCGCTCGGAAGCTCTAAAGGAGGAGATCGAATTTCTTCTGAAAGGATTCGCG 453
Qy 1699 ACGGGAGAACGATATTCGCAAGCGGAAACGCGCATATACCGGCACTTTGGGAGGCG 1758
Db 454 ACGGGAGAACGATATTCGCAAGAACCGGAAAGACATATACCGGCACTTTGGGAGGCG 513

	Query Match	7.5%	Score 169.2;	DB 17;	Length 3300;
	Best Local Similarity	77.5%;	Pred. No. 9.1e-31;		
	Matches 248;	Conservative	0;	Mismatches 33;	Indels 39; Gaps 2;
Qy	1943	CTCGGGAGAGCGGCATCAATCTTTTCGGGAATGGTTTCACCGACCCCAAAACATTTCCAAG	2002		
Db	1	CTCGGGATACCGGCATCAATCTTTTCGGGAATGGTTTCGACTTAATCTCTCAAAGTTTCAAG	60		
Qy	2003	CTAGTAATCTTCGTGTAGACGAGGATTTTACGSCCCGCGGCGCGGAATTTGGGCGGTA	2062		
Db	61	CCGACAAATCTCTTGTGAACGGCGCGGCTTTTACGCGCCGCGAGCGCGCGGATTTGGCGGCA	120		

[illegible]

RESULT 10
US-10-087-192-49
; Sequence 49, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: MORRIS, David W.


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RESULT 15
US-10-101-487-71
; Sequence 71, Application US/10101487
; Publication No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOEQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (522)
US-10-101-487-71

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